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SEARCH REQUEST FORM

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pat. 1, 6-8

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OM protein - protein search, using SW model

Run on: December 9, 2004, 08:39:26 ; Search time 5.05036 Seconds
(without alignments)
923.396 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVLCQCFM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
1	67	100.0	13	AA03165	Aa03165 Linker us
2	67	100.0	13	AAU11643	Aa111643 Interleuk
3	67	100.0	13	ABG70576	Abg70576 Secreted
4	67	100.0	13	ABR44230	Ab44230 Linker pe
5	67	100.0	21	AA125368	Aa125368 IFNAR2/IF
6	67	100.0	34	AA125369	Aa125369 IFNAR2/IF
7	62.7	62.7	360	ABO70163	Ab070163 Pseudom
8	61.2	61.2	199	AA137561	Aa137561 Protein 1
9	61.2	61.2	291	ADM98607	Adm98607 Geranylge
10	61.2	61.2	623	ABR53138	Ab53138 Protein s
11	61.2	61.2	623	ADK63100	Adk63100 Disease t
12	61.2	61.2	640	ABO78796	Ab078796 Pseudom
13	61.2	61.2	920	AA66456	Aa66456 Protein e
14	61.2	61.2	920	ABR5195	Ab5195 Nucleotid
15	60.7	59.7	57	AAU51976	Aa51976 Propionib
16	60.7	59.7	57	ABM48495	Abm48495 Propionib
17	60.7	59.7	171	ABO83978	Ab083978 Pseudom
18	60.7	59.7	406	ABM65541	Abm65541 Propionib
19	60.7	59.7	805	ABR61739	Ab61739 Drosophi
20	60.7	59.7	875	ADJ69760	Adj69760 Human hea
21	60.7	59.7	220	AA11027	Aa11027 H. pylori
22	60.7	59.7	220	AAW98208	Aaw98208 H. pylori
23	60.7	59.7	220	AA117195	Aa117195 H. pylori
24	60.7	59.7	419	ABU22234	Abu22234 Protein e
25	60.7	59.7	450	AD86082	Ad86082 Streptomy

26	39	58.2	770	6	ABR53218	Ab53218 Protein s
27	39	58.2	770	7	ADK63726	Adk63726 Disease t
28	39	58.2	810	6	ABJ26177	Abj26177 Apep911
29	39	58.2	811	6	ABJ25577	Abj25577 Apep911
30	38.5	57.5	903	7	ABO76231	Ab076231 Pseudom
31	38	56.7	191	3	AA355239	Aa355239 Zea mays
32	38	56.7	192	3	AA355238	Aa355238 Zea mays
33	38	56.7	202	3	AA40537	Aa40537 Arabidops
34	38	56.7	202	3	AA40531	Aa40531 Arabidops
35	38	56.7	249	3	AA40536	Aa40536 Arabidops
36	38	56.7	249	3	AA40530	Aa40530 Arabidops
37	38	56.7	249	3	AA355237	Aa355237 Zea mays
38	38	56.7	249	4	ABR62955	Ab62955 Drosophi
39	38	56.7	249	4	ABR65352	Ab65352 Drosophi
40	38	56.7	249	8	ADN73077	Adn73077 Thale cre
41	38	56.7	287	3	AA40535	Aa40535 Arabidops
42	38	56.7	289	3	AA40529	Aa40529 Arabidops
43	38	56.7	384	4	AAU63834	Aau63834 Propionib
44	38	56.7	384	6	ABM60353	Abm60353 Propionib
45	38	56.7	388	3	AA13358	Aa13358 Arabidops

ALIGNMENTS

RESULT 1	AA03165	AA03165 standard; protein; 13 AA.
XX	AA03165;	
AC	AA03165;	
XX		
DT	11-JUN-1999 (first entry)	
XX		
DE	Linker used in Chimeric sIL-6R/IL-6 protein.	
XX		
KW	Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;	
KW	chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;	
KW	highly malignant cancer cell; in vivo engraftment; mammalian cancer;	
KW	human hematopoietic cell; bone marrow transplantation; mammalian cancer;	
KW	hepatotoxic agent protection; haematopoiesis; liver disorder;	
XX	neurological disorder.	
XX		
OS	Synthetic.	
XX		
PN	MO9902552-A2.	
XX		
PD	21-JAN-1999.	
XX		
PF	09-JUL-1998; 98WO-IL000321.	
XX		
PR	10-JUL-1997; 97IL-00121284.	
PR	30-DEC-1997; 97IL-00122818.	
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Revel M, Chebath J, Lapidot T, Kollet O;	
XX		
DR	WPI; 1999-120776/10.	
XX		
PT	New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.	
PT	treating cancers, bone marrow transplantation, increasing haematopoiesis	
PT	or treating liver or neurological disorders.	
XX		
PS	Claim 5; Page 54; 77pp; English.	
XX		
CC	This sequence represents a linker that can be used in the chimeric	
CC	glycosylated soluble interleukin-6 receptor (sIL-6R)-interleukin-6 (IL-6)	
CC	protein (sIL-6R/IL-6) of the invention. The sIL-6R/IL-6 protein comprises	
CC	a fusion protein product between all of the naturally occurring form of	
CC	sIL-6R and all of the naturally occurring form of IL-6, the sIL-6/IL-6	
CC	and analogues being glycosylated in a similar fashion to the	
CC	glycosylation of naturally occurring sIL-6R and IL-6. The sIL-6R/IL-6 and	
CC	analogues are capable of inhibiting the growth of highly malignant cancer	

CC cells, e.g. melanoma cells, eliciting the in vivo engraftment of human
 CC haematopoietic cells in bone marrow transplantation and protecting liver
 CC from hepatotoxic agents. They can be used for the preparation of a
 CC medicament for treating mammalian cancers by way of inhibition of cancer
 CC cells, for enhancement of bone marrow transplantation by way of eliciting
 CC engraftment of human haematopoietic cells in bone marrow transplantation,
 CC for increasing haematopoiesis, for treating liver or neurological
 CC disorders, or in other applications in which IL-6 or IL-6R are used
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00045;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 1 EFGAGLVGGQFM 13

RESULT 2

ID AAU11643 standard; protein; 13 AA.

AC AAU11643;

DT 12-MAR-2002 (first entry)

DE Interleukin 18 (IL-18)/immunoglobulin, linker peptide.

KM Interleukin 18; IL-18; cytokine; interleukin-18 inhibitor;
 KM atherosclerosis; cardiant; vasotropic; antilucer; myocardial infarction;
 KM atherosclerotic plaque; thrombosis of atherosclerotic plaque; stroke;
 KM ischemic syndrome; heart failure; arteriosclerosis; vascularisation;
 KM atheroma; immunoglobulin, linker peptide.

XX Synthetic.

OS WO200185201-A2.

PN 15-NOV-2001.

PD 30-APR-2001; 2001WO-EP004843.

PF 05-MAY-2000; 2000EP-00109606.

PR (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV,
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Chvatchko Y, Tedgui A, Mallat Z;

DR WPI; 2002-075227/10.

PT Use of interleukin-18 inhibitor for manufacture of medicament for
 PT treatment and/or prevention of atherosclerosis, thrombosis of
 PT atherosclerotic plaque, atherosclerotic plaque ulcer and heart failure
 PT recurrent events.

PS Disclosure; Page 16; 54pp; English.

XX The invention describes the use of interleukin-18 (IL-18) inhibitor for
 CC manufacture of medicament for treatment and/or prevention of diseases or
 CC diseased conditions of the arteries, heart failure recurrent events, or
 CC as diagnostic marker for bad clinical prognosis in heart failure or
 CC recurrent events after first event of heart failure or
 CC is useful for: the manufacture of a medicament for treatment and/or
 CC prevention of atherosclerosis/arteriosclerosis; the manufacture of a
 CC medicament for treatment and/or prevention of thrombosis of
 CC atherosclerotic plaque (AP), AP ulcer, AP destabilisation (responsible
 CC for stroke), atheroma, ischemic syndromes e.g. myocardial infarction, AP
 CC disruption or heart failure recurrent events e.g. death, recurrent
 CC ischemia, re-vascularisation and progression of atherosclerosis, where
 CC the heart failure is ischaemic or non-ischaemic and as a diagnostic

CC marker for bad clinical prognosis in heart failure or recurrent events
 CC after first event of heart failure. This sequence is an example of a
 CC peptide linker used to create fusion proteins of Interleukin-18 (IL-18)
 CC with all or part of an immunoglobulin, discussed in the invention
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00045;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 1 EFGAGLVGGQFM 13

RESULT 3

ID ABG70576 standard; peptide; 13 AA.

AC ABG70576;

DT 29-NOV-2002 (first entry)

DE Secreted apoptosis-related protein 1 (SARP-1) linker peptide.

KM Secreted apoptosis-related protein 1; SARP-1; scleroderma;
 KM systemic sclerosis; fibrotic disease; liver cirrhosis; keloid;
 KM interstitial pulmonary fibrosis; Dupuytren's contracture; scarring;
 KM wound healing; postoperative adhesion; reactive fibrosis;
 KM chronic heart failure; myocardial infarction; inflammatory disorder;
 KM lung inflammation; idiopathic pulmonary fibrosis; systemic disease;
 KM rheumatoid arthritis; anti-sclerotic; immunoglobulin.

XX Synthetic.

OS WO200246225-A2.

PN 13-JUN-2002.

PD 30-NOV-2001; 2001WO-EP013992.

PF 06-DEC-2000; 2000EP-00126771.

PR 17-AUG-2001; 2001EP-00118888.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Plater-Zyberk C, Power C, Collinge J;

DR WPI; 2002-706807/76.

PT Use of human Secreted Apoptosis-Related Protein (SARP)-1 and SARP-1
 PT nucleic acids for the treatment of sclerosis, especially systemic
 PT sclerosis.

PS Disclosure; Page 15; 63pp; English.

XX The present invention relates to the use of human secreted apoptosis-
 CC related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which
 CC stimulates the release or potentiates the activity of endogenous SARP-1
 CC for the treatment of scleroderma. The SARP-1 protein binds to and
 CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can
 CC be used in protein therapy, and the polynucleotide sequences encoding
 CC SARP-1 can be used in gene therapy. SARP-1 polypeptide and polynucleotide
 CC sequences, and pharmaceutical compositions comprising SARP-1 are useful
 CC for the treatment of scleroderma, especially systemic sclerosis. They may
 CC also be used to treat fibrotic diseases (e.g. liver cirrhosis,
 CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and
 CC other scarring/wound healing abnormalities), postoperative adhesions and
 CC reactive fibrosis), chronic heart failure (particularly after myocardial
 CC infarction), disorders involving inflammation of the lung (e.g.
 CC idiopathic pulmonary fibrosis), and systemic diseases (e.g. rheumatoid
 CC arthritis). The present sequence represents a linker peptide that can be

CC used to fuse SARP-1 to an immunoglobulin to form a fusion protein
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLVIGGQFM 13
DB 1 EFGAGLVIGGQFM 13

RESULT 4

ABR44230 standard; peptide; 13 AA.

AC ABR44230;

DT 18-AUG-2003 (first entry)

DE Linker peptide used in constructing an IL-6R/IL-6 chimera.

XX IL-6; gp130; interleukin-6; antidiabetic; neuroprotective; gene therapy;
KW linker.

OS Synthetic.

PN WO2003033015-A1.

PD 24-APR-2003.

PF 10-OCT-2002; 2002WO-EP011364.

PR 11-OCT-2001; 2001EP-00123400.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Dreano M, Vitte P;

DR WPI; 2003-403150/38.

XX Use of a substance signaling through gp130, or use of a vector for
XX inducing and/or enhancing endogenous production of interleukin-6 in cell,
PT for preparing a medicament for treating and preventing diabetic
PT neuropathy.

PS Disclosure; Page 17; 85pp; English.

XX The invention relates to the use of a substance (I) signaling through
CC gp130, or use of a vector (II) for inducing and/or enhancing the
CC endogenous production of interleukin-6 (IL-6) in a cell. (I), (II) or a
CC cell expressing (I), is useful in the manufacture of a medicament for the
CC treatment and/or prevention of diabetic neuropathy. (I) is useful for
CC treating or preventing diabetic neuropathy such as polyneuropathy or
CC mononeuropathy. The present sequence represents a linker peptide used for
CC constructing an IL-6R/IL-6 chimera

XX Sequence 13 AA;

Query Match 100.0%; Score 67; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLVIGGQFM 13
DB 1 EFGAGLVIGGQFM 13

RESULT 5

AAV25368 standard; peptide; 21 AA.

XX

AC AAV25368;
XX
XX 06-SEP-1999 (first entry)

DE IFNAR2/IFN-beta complex peptide fragment 11.

XX IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
KW human interferon alpha/beta receptor; anticancer; immunomodulatory;
KW anti-arthritis; antidiabetic; treatment; hepatitis; viral infection;
KW hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
KW diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
KW acquired immune deficiency syndrome.

OS Synthetic.

PN WO9932141-A1.

PD 01-JUL-1999.

PF 18-DEC-1998; 96WO-US026926.

PR 19-DEC-1997; 97US-0068295P.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
(MCIN/) MCINNIS P G.

PI Tepper M, Cunningham M, Sherrie D, El Tayar N, McKenna S;

DR WPI; 1999-405115/34.

XX Prolonging in vivo activity of type I interferon by complexing.

PS Disclosure; Page 80; 86pp; English.

XX This invention describes a novel method for prolonging the in vivo effect
CC of type I interferon (IFN) by administering IFN as a complex (A) with a
CC subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
CC product of the invention has antiviral, anticancer, immunomodulatory,
CC anti-arthritis and antidiabetic activity. (A) have the antiviral,
CC anticancer and immunomodulating activities of IFN, e.g. for treating
CC hepatitis and other viral infections, hairy cell leukemia, Kaposi's
CC sarcoma, multiple myeloma and other cancers, multiple sclerosis,
CC rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
CC deficiency syndrome and lupus. When complexed in (A), the storage life of
CC IFN is increased (i.e. it is stabilized against oligomerization, without
CC the need for storage at acidic pH) and its biological effect is
CC potentiated

XX Sequence 21 AA;

Query Match 100.0%; Score 67; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLVIGGQFM 13
DB 6 EFGAGLVIGGQFM 18

RESULT 6

AAV25369 standard; peptide; 34 AA.

XX AAV25369;

AC AAV25369;

DT 06-SEP-1999 (first entry)

DE IFNAR2/IFN-beta complex peptide fragment 12.

XX IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
KW human interferon alpha/beta receptor; anticancer; immunomodulatory;
KW anti-arthritis; antidiabetic; treatment; hepatitis; viral infection;
KW hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;

KW diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
 KM acquired immune deficiency syndrome.
 XX
 OS Synthetic.
 XX
 PN WO9932141-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-US026926.
 XX
 PR 19-DEC-1997; 97US-0068295P.
 XX
 PA (ISTF) ARS APPLIED RBS SYSTEMS HOLDING NV.
 XX (MCIN/) MCINNIS P G.
 PI
 XX Tepper W, Cunningham M, Sherris D, El Tayar N, McKenna S;
 DR WPI; 1999-405115/34.
 XX
 PT Prolonging in vivo activity of type I interferon by complexing.
 XX
 PS Disclosure; Page 80; 86pp; English.
 XX
 CC This invention describes a novel method for prolonging the in vivo effect
 CC of type I interferon (IFN) by administering IFN as a complex (A) with a
 CC subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
 CC product of the invention has antiviral, anticancer, immunomodulatory,
 CC anti-arthritic and antidiabetic activity. (A) have the antiviral,
 CC anticancer and immunomodulating activities of IFN, e.g. for treating
 CC hepatitis and other viral infections, hairy cell leukemia, Kaposi's
 CC sarcoma, multiple myeloma and other cancers, multiple sclerosis,
 CC rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
 CC deficiency syndrome and lupus. When complexed in (A), the storage life of
 CC IFN is increased (i.e. it is stabilized against oligomerization, without
 CC the need for storage at acidic pH) and its biological effect is
 CC potentiated
 XX
 SQ Sequence 34 AA;
 XX
 Query Match 100.0%; Score 67; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EFGAGLVGGQFM 13
 DB 6 EFGAGLVGGQFM 18
 XX
 RESULT 7
 ABO70163
 ID ABO70163 standard; protein; 360 AA.
 XX
 AC ABO70163;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #2338.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX

XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX WPI; 2003-615309/58.
 DR
 DR N-PsDB; ABD03734.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 18909; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 360 AA;
 XX
 Query Match 62.7%; Score 42; DB 7; Length 360;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GAGLVGGQF 12
 DB 202 GAALVGGQF 211
 XX
 RESULT 8
 AAY37561
 ID AAY37561 standard; protein; 199 AA.
 XX
 AC AAY37561;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE Protein involved in intermediate metabolism of fatty acids.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perilepitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis.
 XX
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB001939.
 XX
 PR 28-NOV-1997; 97FR-00015041.
 XX 17-DEC-1997; 97FR-00016034.
 XX 04-NOV-1998; 98US-0107077P.
 XX
 PA (BEST) GENSET.
 XX
 PI Griffiths R;
 XX
 DR WPI; 1999-371125/31.
 XX

[illegible]

CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM
XX
SQ Sequence 623 AA;

Query Match 61.2%; Score 41; DB 6; Length 623;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
Db 194 EFGASVLAGQ 204

RESULT 11
ADK63100
ID ADK63100 standard; protein; 623 AA.

XX ADK63100;

DT 06-MAY-2004 (first entry)

DE Disease treating protein complex-derived protein #676.

XX protein complex; drug target; diagnosis.

XX Unidentified.

XX EPI338608-A2.

XX 27-AUG-2003.

XX 20-DEC-2002; 2002EP-00102902.

XX 20-DEC-2001; 2001EP-00130253.

XX (CELL-) CELLZONE AG.

PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;

PI Marzloch M, Grandi P, Krause R, Krause U, Merino A, Bauch A;

PI Michon A, Leutwein C, Rick J;

DR WPI; 2003-638460/61.

XX N-PSDB; ADK63101.

PT New proteins and protein complexes from eukaryotes, useful as targets in

PT drug screening, or in diagnosing or screening for the presence of a

PT disease or disorder, or a predisposition for developing a disease or

PT disorder in a subject.

XX Disclosure; SEQ ID NO 1351; 13pp; English.

XX The invention relates to novel protein complexes comprising a first and a

XX second protein, or its derivative, fragment, homologue or variant. The

XX proteins are selected from given protein complexes, which are not defined

XX in the specification. The variants are encoded by nucleic acids that

XX hybridize to the nucleic acids encoding the proteins under low stringency

XX conditions. The protein complexes are useful as targets for an active

XX agent of a pharmaceutical. These protein complexes are particularly

XX useful as drug targets for the treatment or preventing of a disease or

XX disorder. The complexes and methods above are useful in diagnosing or

XX screening for the presence of a disease or disorder or a predisposition

XX for developing a disease or disorder in a subject. These are also useful

XX in screening for a drug for treatment or prevention of a disease or

XX disorder. The molecule that modulates the amount, activity or protein

XX components of the complex is useful for the manufacture of a medicament

XX for the treatment or prevention of a disease or disorder. This sequence

XX corresponds to a protein of the invention. (Note: the sequence data for

XX this patent did not form part of the printed specification but was

XX obtained from the EPO in electronic format.)

XX Sequence 623 AA;

Query Match 61.2%; Score 41; DB 7; Length 623;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
Db 194 EFGASVLAGQ 204

RESULT 12
ABO78796
ID ABO78796 standard; protein; 640 AA.

XX ABO78796;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #10971.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD12367.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

PT useful as molecular targets for diagnostics, prophylaxis and treatment of

PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 27542; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the

XX polynucleotides encoding them. The sequences are useful in diagnosis and

XX therapy of pathological conditions, as molecular targets for diagnostics,

XX prophylaxis and treatment of pathological conditions resulting from a

XX bacterial infection, for evaluating a compound, such as a polypeptide,

XX for the ability to bind a P. aeruginosa nucleic acid, as components of

XX effective antibacterial targets, as targets for antibacterial drugs,

XX including anti-P. aeruginosa drugs, as templates for recombinant

XX production of P. aeruginosa-derived peptides or polypeptides, as target

XX components for diagnosis and/or treatment of P. aeruginosa-caused

XX infection, and in detection of P. aeruginosa sequences or other sequences

XX of Pseudomonas species using biochip technology. Sequences ABO67826-

XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The

XX sequence data for this patent did not form part of the printed

XX specification but was obtained in electronic format from USPTO at

XX seqdata.uspto.gov/sequence.html

XX Sequence 640 AA;

XX Query Match 61.2%; Score 41; DB 7; Length 640;

XX Best Local Similarity 80.0%; Pred. No. 4.1e+02;

XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 2 EFGAGLVGGQ 11

XX Db 304 FAAGLALGGQ 313

RESULT 13

AB66456 standard; protein; 920 AA.

09-APR-2001 (first entry)

Protein encoded by *Mycobacterium tuberculosis* mmpL7 (Rv2942) gene.

Mycobacterium tuberculosis; attenuated microorganism; mmpL7; Rv2942;

signature tagged transposon mutant; mutant library;

Mycobacterium tuberculosis; actinomycetales; antibacterial; immunostimulant;

vacine.

11-JAN-2001.

06-JUL-2000; 2000MO-IB000950.

06-JUL-1999; 99US-0142982P.

08-JUL-1999; 99US-0142833P.

(INSP) INST PASTER.

Glequel B, Guillhot C, Camacho L;

WPI; 2001-091804/10.

N-PSDB; AAF31617.

Screening a mutant library for mutants unable to grow under specific

conditions and for identifying loci involved in pathogenicity, comprises

using signature tagged transposon mutagenesis.

Example 8; Fig 14A; 159pp; English.

The present sequence is given in a specification relating to a method for

screening a library of mutants. The method comprises constructing a

library with insertions in genes and/or regulatory regions of the

organisms of interest, where the insertion contains a tag and/or a

transposon associated with a tag. The mutants are identified by

hybridisation of the tags to known sequences. The method is useful for

treating an individual suffering from a mycobacterial infection,

suspected of being infected with a *Mycobacterium*, or having been exposed

to an infectious *Mycobacterium*. It is also useful for identifying and

isolating mutants of actinomycetales and for identifying compounds that

have antibiotic activity. The method is used to identify mutants of

microorganisms, preferably an actinomycetales, such as *M. tuberculosis*,

M. bovis, *M. leprae*, *M. avium*, *M. intracellulare* and *M.*

paratuberculosis, that is unable to grow under specific conditions. It is

especially useful for identifying loci involved in pathogenicity. It is

useful in constructing vaccines. The method can be used to screen

multiple libraries concurrently. It can screen libraries of different

organisms or different strains of the same organism. The present protein

is encoded by a gene which is disrupted by the insertion of the IS 1096

transposon to produce an attenuated mutant of *Mycobacterium tuberculosis*

Sequence 920 AA;

RESULT 14

ABR5195 standard; protein; 920 AA.

29-JUL-2003 (first entry)

Nucleotide sequence of gene down-regulated during nutrient starvation.

Carbon starvation; nutrient-starving culture; *Mycobacterium*; vaccine;

Mycobacterium tuberculosis; transmembrane transport protein mmpL7.

Mycobacterium tuberculosis.

MO2003035661-A2.

01-MAY-2003.

21-OCT-2002; 2002MO-GB004718.

24-OCT-2001; 2001GB-00025535.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

James BW, Marsh P, Hampshire T;

WPI; 2003-421402/39.

N-PSDB; ACC43891.

New isolated mycobacterial peptides, useful for the manufacture of a

medicament for treating or preventing a mycobacterial infection.

Claim 4; Page 117-121; 138pp; English.

The present sequence is transmembrane transport protein mmpL7. It is

encoded by a gene which is down-regulated during survival under carbon

starvation and oxygen limitation conditions. The specification describes

mycobacterial genes which are down-regulated during a stationary phase

culture of mycobacteria under nutrient-starving culture conditions, when

compared with an exponential phase culture of mycobacteria under culture

conditions that are not nutrient-starving and that support exponential

growth of the mycobacteria. Mycobacterial polypeptides which are down-

regulated under nutrient-starving conditions are useful for the

manufacture of a medicament for treating or preventing a mycobacterial

infection. They may also be useful as vaccines

Sequence 920 AA;

Query Match

Best Local Similarity 76.9%; Score 41; DB 6; Length 920;

Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

2 FGAGLVL--GGQF 12

876 FGAGLVLVSGGSF 888

RESULT 15

AAU51976

AAU51976 standard; protein; 57 AA.

27-FEB-2002 (first entry)

Propionibacterium acnes immunogenic protein #12872.

SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;

uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

XX PN WO200181581-A2.
 XX XX 01-NOV-2001.
 PD XX
 PF 20-APR-2001; 2001WO-US012865.
 XX XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX XX
 PA (CORI-) CORIXA CORP.
 XX XX
 PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A,
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D,
 DR N-PSDB; AAS59553.
 DR WPI; 2001-616774/71.
 XX XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX XX
 PS Example 1; SEQ ID NO 13171; 1069pp; English.
 XX XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX XX
 SQ Sequence 57 AA;
 XX XX
 Query Match 59.7%; Score 40; DB 4; Length 57;
 Best Local Similarity 80.0%; Pred. NO. 47;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FGAGLVYGGQ 11
 Db 43 FGAGLVYAGQ 52
 XX XX
 RESULT 16
 ID ABM48495 standard; protein; 57 AA.
 XX XX
 AC ABM48495;
 XX XX
 DT 20-OCT-2003 (first entry)
 XX XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #13171.
 XX XX
 KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KM immunostimulant; immune response; vaccine.
 XX XX
 OS Propionibacterium acnes.
 XX XX
 PN WO2003033515-A1.

XX XX 24-APR-2003.
 PD XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX XX
 PR 15-OCT-2001; 2001US-00978825.
 XX XX
 PA (CORI-) CORIXA CORP.
 XX XX
 PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL,
 PI Zhang Y, Wang S, Jen S, Lodes WD, Benson DR, Jones R, Carter D,
 PI Barth B, Valiieve-Douglas J;
 XX XX
 DR WPI; 2003-381769/36.
 DR N-PSDB; ACF64482.
 XX XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX XX
 PS Example 1; SEQ ID NO 13171; 1481pp; English.
 XX XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX XX
 SQ Sequence 57 AA;
 XX XX
 Query Match 59.7%; Score 40; DB 6; Length 57;
 Best Local Similarity 80.0%; Pred. NO. 47;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FGAGLVYGGQ 11
 Db 43 FGAGLVYAGQ 52
 XX XX
 RESULT 17
 ID ABO83978 standard; protein; 171 AA.
 XX XX
 AC ABO83978;
 XX XX
 DT 29-JUL-2004 (first entry)
 XX XX
 DE Pseudomonas aeruginosa polypeptide #16153.
 XX XX
 KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX XX
 PN

OS Pseudomonas aeruginosa.
 XX
 XX US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 PI MPI: 2003-615309/58.
 DR N-PSDB; ABD17549.
 DR
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 32724; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 CC
 XX
 SQ Sequence 171 AA;
 XX

Query Match 59.7%; Score 40; DB 7; Length 171;
 Best Local Similarity 77.8%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 2;

QY 2 FGAGLVLTGG 10
 ||:|||||
 DB 101 FGSGULTGG 109

RESULT 18
 ABM65541
 ID ABM65541 standard; protein; 406 AA.
 AC ABM65541;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes immunogenic polypeptide #30217.
 XX
 KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KM immunostimulant; immune response; vaccine; immunogenic.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX

PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallsve-Douglas J;
 XX
 DR MPI: 2003-381789/36.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Claim 7; SEQ ID NO 30217; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed P. acnes polypeptide which is
 CC thought to contain an immunogenic region. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX

Query Match 59.7%; Score 40; DB 6; Length 406;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

QY 2 FGAGLVLTGG 11
 |||||
 DB 392 FGAGLVYAGQ 401

RESULT 19
 ABB61739
 ID ABB61739 standard; protein; 805 AA.
 AC ABB61739;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 12009.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX

XX 23-MAR-2001; 2001WO-US009231.
PF 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
PR
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI MPI; 2001-656860/75.
XX N-PSDB; ABL05842.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PS Disclosure; SEQ ID NO 12009; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 805 AA;

Query Match 59.7%; Score 40; DB 4; Length 805;
Best Local Similarity 54.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EFAGGLVIGGQ 11
: |||||:
Db 172 DFGAGLIGGK 182

RESULT 20
ADJ69760
ID ADJ69760 standard; protein; 875 AA.
XX
AC ADJ69760;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target Segid1566.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
PI MPI; 2003-845369/78.
DR
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1566; 180pp; English.
PS
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 875 AA;

Query Match 59.7%; Score 40; DB 7; Length 875;
Best Local Similarity 54.5%; Pred. No. 8.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EFAGGLVIGGQ 11
: |||||:
Db 169 DFGAGLIGGK 179

RESULT 21
AAV11027
ID AAV11027 standard; protein; 220 AA.
XX
AC AAV11027;
XX
DT 08-JUN-1999 (first entry)
XX
DE H. pylori ORF 029e41622_34176513_c1_50 outer membrane protein.
XX
KW Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;
KW cytoplasmic protein; cellular protein.
XX
OS Helicobacter pylori.
XX
PN WO9824475-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-US022104.
XX
XX 05-DEC-1996; 96US-00759625.
PR 25-MAR-1997; 97US-00823745.
PR 14-JUL-1997; 97US-00891928.
XX
XX (ASTR) ASTRA AB.
XX
XX Smith D, Alm RA, Doig PC, Kabok Z, Castriciotta LM,
PI MPI; 1998-333051/29.
XX
XX N-PSDB; AAX30556.
XX
XX New isolated Helicobacter pylori nucleic acids - used to develop products
PT

CC This sequence represents a *Helicobacter pylori* GHPD protein of the CC invention. The polypeptides can be used for preventing or treating CC *Helicobacter* infections, and gastrointestinal diseases associated with CC these infections, including acute, chronic, and atrophic gastritis, and CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be CC used for the production of antibodies. The products can also be used for

RESULT 24
ABU22234
ID ABU22234 standard; protein; 419 AA

AC ABU22234;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #7761.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Burkholderia mallei.
 XX
 PN W0200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA26104.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 50158; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 419 AA;

Query Match 58.2%; Score 39; DB 6; Length 419;
 Best Local Similarity 61.5%; Pred. No. 5.5e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ERGAGLVGGQFM 13
 DB 254 ERGAEIIDGGPFW 266

RESULT 25
 ADE86082
 ID ADE86082 standard; protein; 450 AA.
 XX
 AC ADE86082;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Streptomyces hygroscopicus efflux protein.
 XX
 KW antibiotic; AC98; efflux protein.
 XX
 OS Streptomyces hygroscopicus.
 XX
 PN W02003082909-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 28-MAR-2003; 2003WO-US009746.
 PF 29-MAR-2002; 2002US-0368713P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Hucul JA, Macgarvey N, Greenstein M;
 PI WPI; 2003-812536/76.
 DR N-PSDB; ADE86070.
 XX
 PT New non-ribosomal peptide synthetase, useful for preparing antibacterial
 PT peptides, derived from Streptomyces, also related nucleic acid and
 PT modified antibiotics.
 XX
 PS Claim 10; SEQ ID NO 30; 163pp; English.
 XX
 CC The present sequence is the protein sequence of an efflux protein thought
 CC to be involved in the biosynthesis of the peptide antibiotic AC98 of
 CC Streptomyces hygroscopicus NS17 (NRRL 30439). The sequence is predicted
 CC from an open reading frame (ORF10) in a gene cluster ADE86070 isolated
 CC from NS17, which includes a non-ribosomal peptide synthetase (NRPS)
 CC complex. Sequence comparisons of specific ORPs indicated that the encoded
 CC proteins are tailoring enzymes involved in modification of the AC98
 CC peptide core, e.g. glycosylation, methylation or acylation, or in
 CC resistance. The invention provides a method of producing a cyclic
 CC transformed host cells. It also provides a method of producing a cyclic
 CC peptide antibiotic, such as AC98, using the NRPS comprised of mpba
 CC ADE86071 and mpba ADE86072. The antibiotic is preferably a
 CC lipoglycopeptide antibiotic with activity against Gram-positive
 CC pathogens. Also provided are methods of modifying NRPS to produce an
 CC antibiotic having a modified peptide core, and a method for evaluating
 CC the structural regions of the modified peptide.
 XX
 SQ Sequence 450 AA;

Query Match 58.2%; Score 39; DB 7; Length 450;
 Best Local Similarity 72.7%; Pred. No. 5.9e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ERGAGLVGGQFM 12
 DB 305 ERGAGLVGGQFM 315

RESULT 26
 ABR53218
 ID ABR53218 standard; protein; 770 AA.
 XX

AC ABR53218;
 XX
 DT 20-JUN-2003 (first entry)
 XX
 DE Protein sequence #SEQ ID 1301.
 XX
 KM Multiprotein complex; eukaryote; drug target; diagnosis.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN EP1258494-A1.
 XX
 PD 20-NOV-2002.
 XX
 PF 20-DEC-2001; 2001EP-00130253.
 XX
 PR 15-MAY-2001; 2001EP-00111774.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 PI Marzloch M, Schultz JD, Superti-Furga G;
 XX
 DR WPI; 2003-250078/25.
 DR N-PSDB; ACC61260.
 XX
 PT New isolated protein complexes useful for diagnosing a disease or
 disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease or
 disorder.
 PS Disclosure; SEQ ID NO 1301; 17pp + Sequence Listing; English.
 XX
 CC The invention relates to multiprotein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR53568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this
 CC patent is not represented in the printed specification, but is based on
 CC sequence information supplied by the European Patent Office. The complete
 CC document is available on CD-ROM
 CC
 SQ Sequence 770 AA;
 QY
 Query Match 58.2%; Score 39; DB 6; Length 770;
 Best Local Similarity 70.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 142 FSAAGLVIGGK 151
 QY 2 FGAGLVIGGQ 11
 ID ABR53218
 ID ADK63726 standard; protein; 770 AA.
 XX
 AC ADK63726;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Disease treating protein complex-derived protein #790.
 XX
 KM protein complex; drug target; diagnosis.
 XX
 OS Unidentified.
 XX
 PN EP1338608-A2.
 XX

PD 27-AUG-2003.
 XX
 PF 20-DEC-2002; 2002EP-00102902.
 XX
 PR 20-DEC-2001; 2001EP-00130253.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK63727.
 XX
 PT New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.
 PS Disclosure; SEQ ID NO 1579; 13pp; English.
 XX
 CC The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drug targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).
 CC
 SQ Sequence 770 AA;
 QY
 Query Match 58.2%; Score 39; DB 7; Length 770;
 Best Local Similarity 70.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 142 FSAAGLVIGGK 151
 QY 2 FGAGLVIGGQ 11
 ID ABR53218
 ID ABJ26177 standard; protein; 810 AA.
 XX
 AC ABJ26177;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Aspergillus fumigatus essential gene protein #835.
 XX
 KM Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KM cancer; contamination; biofilm; antibody; immune response.
 XX
 OS Aspergillus fumigatus.
 XX
 PN WO2002086090-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013142.
 XX

XX US6551795-B1.
PN 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI MPI: 2003-615309/56.
XX N-PSDB; ABD09802.
DR Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 24977; 455pp; English.
PS
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polymucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences AB067826-
CC AB084396 represent *P. aeruginosa* polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 903 AA;
Query Match 57.5%; Score 38.5; DB 7; Length 903;
Best Local Similarity 64.3%; Pred. No. 1.5e+03;
Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
QY 2 FGAG--LVLGQGF 12
Db 509 FGAGPAAALGGGF 522
RESULT 31
AAG35239
ID AAG35239 standard; protein; 191 AA.
XX AAG35239;
AC
XX 18-OCT-2000 (first entry)
DT
XX Zea mays protein fragment SEQ ID NO: 43019.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.
XX Zea mays subsp. mays.
OS
XX
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-00301439.
PF
XX

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128334P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
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PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140655P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
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PR 20-JUL-1999; 99US-0144336P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
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PR 21-JUL-1999; 99US-0145087P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145919P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147319P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
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PR 20-AUG-1999; 99US-0149723P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 27-AUG-1999; 99US-0151303P.
PR 30-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153788P.
PR 13-SEP-1999; 99US-0154018P.
PR 15-SEP-1999; 99US-0154039P.
PR 16-SEP-1999; 99US-0154779P.
PR 20-SEP-1999; 99US-0155139P.
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PR 23-SEP-1999; 99US-0155659P.
PR 24-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 29-SEP-1999; 99US-0156596P.

PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 56.7%; Score 38; DB 3; Length 191;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FGAGVILGG 10
Db 74 FGCGVILGG 82

RESULT 32

ID AAG35238 standard; protein; 192 AA.

AC AAG35238;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 43018.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

OS Zea mays subsp. mays.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.

PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
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PR	05-MAY-1999;	99US-0132485P.
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PR	30-JUN-1999;	99US-0141287P.
PR	01-JUL-1999;	99US-0141842P.
PR	01-JUL-1999;	99US-0142154P.
PR	02-JUL-1999;	99US-0142055P.
PR	06-JUL-1999;	99US-0142390P.
PR	08-JUL-1999;	99US-0142803P.
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PR	12-JUL-1999;	99US-0142977P.
PR	13-JUL-1999;	99US-0143542P.
PR	14-JUL-1999;	99US-0143624P.
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PR	16-JUL-1999;	99US-0144085P.
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PR	23-JUL-1999;	99US-0145224P.
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PR	27-JUL-1999;	99US-0145913P.
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PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0145951P.
PR	02-AUG-1999;	99US-0146386P.
PR	02-AUG-1999;	99US-0146387P.
PR	02-AUG-1999;	99US-0146388P.
PR	03-AUG-1999;	99US-0147038P.
PR	04-AUG-1999;	99US-0147204P.
PR	05-AUG-1999;	99US-0147302P.
PR	05-AUG-1999;	99US-0147192P.
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PR	06-AUG-1999;	99US-0147303P.
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PR	09-AUG-1999;	99US-0147932P.
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PR	13-AUG-1999;	99US-0148565P.
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PR	17-AUG-1999;	99US-0149175P.
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PR	23-AUG-1999;	99US-0149930P.
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PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
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PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158022P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.

PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 56.7%; Score 38; DB 3; Length 192;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FGAGIVLCG 10
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Db 75 FGCEVILCG 83

RESULT 33

AA640537 standard; protein; 202 AA.

AA640537;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 50309.

Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
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PR 31-AUG-1999; 99US-015138P.
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PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
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PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 56.7%; Score 38; DB 3; Length 202;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
Db 85 FGCGVILGG 93

RESULT 34

ID AAG04531 standard; protein; 202 AA.

AC AAG04531;

DT 17-OCT-2000 (First entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 591.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 56.7%; Score 38; DB 3; Length 202;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FGAGLVVGG 10
Db 85 FCGCVILGG 93

RESULT 35
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ID AAC40536 standard; protein; 249 AA.
XX AAC40536;
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XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50308.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
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Query Match 56.7%; Score 38; DB 3; Length 249;
Best local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 2 FGAGIVTGG 10
Db 132 FGCGVING 140

RESULT 36
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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Query Match 56.7%; Score 38; DB 3; Length 249;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVIGG 10
 Db 132 FGCGVILGG 140

RESULT 37
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AC AAG35237;
 XX 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 43017.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence; corn.

XX Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

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Query Match 56.7%; Score 38; DB 3; Length 249;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FGAGLVGG 10
 DB 132 FCGGVILGG 140

RESULT 38
 ABB62955
 ID ABB62955 standard; protein; 249 AA.
 XX
 AC ABB62955;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15657.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07058.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 PS
 PS Disclosure; SEQ ID NO 15657; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 249 AA;
 Query Match 56.7%; Score 38; DB 4; Length 249;
 Best Local Similarity 70.0%; Pred. No. 4.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 AGVLGGGGM 13
 DB 92 AGVLGGGLI 101
 RESULT 39
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 ID ABB65352 standard; protein; 249 AA.
 XX
 AC ABB65352;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 22848.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.

XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li FWD, Myers EW,
 XX DR WPI; 2001-656660/75.
 XX DR N-PSDB; ABL09455.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
 XX PT interactions.
 XX PS Disclosure; SEQ ID NO 22848; 21pp + Sequence listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signaling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX CC sequences (ABL1840-ABL16175) and the encoded proteins (AB57737-
 XX CC AB572072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 249 AA;
 QY Query Match 56.7%; Score 38; DB 4; Length 249;
 Db Best Local Similarity 70.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1;
 4 AGTATGGGFM 13
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 92 AGTATGGQLI 101
 RESULT 40
 ADN73077 standard; protein; 249 AA.
 AC ADN73077;
 XX DT 15-JUL-2004 (first entry)
 XX DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 972.
 XX DE plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 XX KW animal feed product; thale cress; cell wall biosynthesis;
 XX KW nitrogen metabolism; carbon metabolism.
 XX OS Arabidopsis thaliana.
 XX PN WO2004035798-A2.
 XX PD 29-APR-2004.
 XX PF 20-OCT-2003; 2003WO-EP011658.
 XX PR 18-OCT-2002; 2002EP-00079408.
 XX PA (CROP-) CROPDESTIGN NV.
 XX

PI Inze D, De Veylder L, Vlieghe K;
 XX DR WPI; 2004-348466/32.
 XX DR N-PSDB; ADN73076.
 XX PT Altering plant characteristics, useful for producing plants for enzyme or
 XX PT pharmaceutical production comprising modifying in a plant, expression of
 XX PT one or more nucleic acids and/or modifying level or activity of one or
 XX PT more proteins.
 XX PS Claim 1; SEQ ID NO 972; 134pp; English.
 XX CC This invention relates to a novel method for altering one or more plant
 XX CC characteristics. Specifically, it refers to identifying genes that are up
 XX CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 XX CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 XX CC alter plant characteristics accordingly. The present invention describes
 XX CC generating transgenic plants for the production of growth regulators,
 XX CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 XX CC the altered plant characteristics are selected from increased yield or
 XX CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 XX CC or physiology, altered endoreduplication, biochemistry, signal
 XX CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 XX CC each relative to the corresponding wild type plants. Accordingly, these
 XX CC sequences can also be useful as positive or negative selectable markers
 XX CC during transformation of cells or tissues. The identified genes play a
 XX CC role in a variety of biological processes such as DNA replication, cell
 XX CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 XX CC transcription factors. This polypeptide sequence is thale cress protein
 XX CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 XX CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 XX CC invention.
 XX SQ Sequence 249 AA;
 QY Query Match 56.7%; Score 38; DB 8; Length 249;
 Db Best Local Similarity 66.7%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1;
 2 FGAGTATGG 10
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 132 FGCGTATGG 140
 Search completed: December 9, 2004, 09:16:30
 Job time : 9.05036 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 09:21:02 ; Search time 4.58273 Seconds
(without alignments)
1013.220 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVIGGQFM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	61.2	97	US-10-424-599-197757 Sequence 197757, A
3	41	61.2	291	US-10-041-018-27 Sequence 27, Appl
4	41	61.2	319	US-10-156-761-9015 Sequence 9015, Ap
5	40	59.7	875	US-10-408-765A-1566 Sequence 1566, Ap
6	39	58.2	178	US-10-335-977-5090 Sequence 5090, Ap
7	39	58.2	220	US-09-881-752A-16 Sequence 16, Appl
8	39	58.2	220	US-10-335-977-5091 Sequence 5091, Ap
9	39	58.2	403	US-10-425-114-48433 Sequence 48433, A
10	39	58.2	405	US-10-425-114-41675 Sequence 41675, A
11	39	58.2	405	US-10-425-114-48462 Sequence 48462, A
12	39	58.2	405	US-10-425-114-49554 Sequence 49554, A
13	39	58.2	419	US-10-282-122A-50158 Sequence 50158, A

14	39	58.2	450	US-10-402-842-30 Sequence 30, Appl
15	39	58.2	528	US-10-369-493-21791 Sequence 21791, A
16	39	58.2	545	US-10-156-761-11459 Sequence 11459, A
17	39	58.2	748	US-10-369-493-3245 Sequence 3245, Ap
18	39	58.2	770	US-10-369-493-22168 Sequence 22168, A
19	39	58.2	8210	US-10-128-714-8235 Sequence 8235, Ap
20	39	58.2	811	US-10-128-714-8235 Sequence 3335, Ap
21	38	56.7	94	US-10-424-599-231652 Sequence 231652, A
22	38	56.7	94	US-10-425-115-265962 Sequence 265962, A
23	38	56.7	102	US-10-425-115-294011 Sequence 294011, A
24	38	56.7	146	US-10-369-493-2228 Sequence 2228, Ap
25	38	56.7	182	US-10-425-115-227826 Sequence 227826, A
26	38	56.7	238	US-10-437-963-203753 Sequence 203753, A
27	38	56.7	241	US-10-425-115-46558 Sequence 46558, A
28	38	56.7	249	US-10-424-599-205502 Sequence 205502, A
29	38	56.7	249	US-10-437-963-174772 Sequence 174772, A
30	38	56.7	249	US-10-425-115-231962 Sequence 231962, A
31	38	56.7	249	US-10-425-115-231963 Sequence 231963, A
32	38	56.7	249	US-10-425-115-283162 Sequence 283162, A
33	38	56.7	249	US-10-425-115-283165 Sequence 283165, A
34	38	56.7	249	US-10-425-115-283167 Sequence 283167, A
35	38	56.7	249	US-10-425-115-283173 Sequence 283173, A
36	38	56.7	249	US-10-425-115-284033 Sequence 284033, A
37	38	56.7	249	US-10-739-930-7930 Sequence 7930, Ap
38	38	56.7	256	US-10-424-599-205503 Sequence 205503, A
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41	38	56.7	270	US-10-425-114-60462 Sequence 60462, A
42	38	56.7	272	US-10-425-115-283158 Sequence 283158, A
43	38	56.7	276	US-10-437-963-140821 Sequence 140821, A
44	38	56.7	287	US-10-425-115-207790 Sequence 207790, A
45	38	56.7	327	US-10-437-963-154362 Sequence 154362, A

ALIGNMENTS

RESULT 1
US-10-425-115-267639
; Sequence 267639, Application US/10425115
; General Information: US20040214272A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267639
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRR4577_175692C.1.pep
US-10-425-115-267639

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Best Local Similarity 63.6% Pred. No. 14;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 36 DYSGGLVIGGQ 46

RESULT 2
US-10-424-599-197757
; Sequence 197757, Application US/10424599
; Publication No. US20040031072A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 19757
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_205C.1.pep
US-10-424-599-19757
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Query Match
Best Local Similarity 61.2%; Score 41; DB 15; Length 97;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 55 FGAGLVGGQF 65
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US-10-041-018-27
; Sequence 27, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US/10023547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-041-018-27
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Query Match
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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 2 FGAGLVGGQF 12
Db 153 FGAGLVGGQF 163
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US-10-156-761-9015
; Sequence 9015, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9015
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9015
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3 GAGLVGGQ 11
Db 143 GAGLVGGQ 151
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RESULT 5
US-10-408-765A-1566
; Sequence 1566, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Brian D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1566
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1566
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Best Local Similarity 59.7%; Score 40; DB 16; Length 875;
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QY 1 EFGAGLVGGQ 11
Db 169 EFGAGLVGGQ 179
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RESULT 6
US-10-335-977-5090
; Sequence 5090, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5090:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5090:
US-10-335-977-5090

Query Match 58.2%; Score 39; DB 15; Length 178;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQFM 13
Db 28 GFGVVLGKRV 38

RESULT 7
US-09-881-752A-16
Sequence 16, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 220
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-881-752A-16

Query Match 58.2%; Score 39; DB 9; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQFM 13
|:|||||:

Db 70 GFGVVLGKRV 80

RESULT 8
US-10-335-977-5091
Sequence 5091, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5091:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...220
SEQUENCE DESCRIPTION: SEQ ID NO: 5091:
US-10-335-977-5091

Query Match 58.2%; Score 39; DB 15; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQFM 13
|:|||||:

RESULT 9
US-10-425-114-4843
Sequence 4843, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48433
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-059-A10_FLI.pep
US-10-425-114-48433
```

```

Query Match          58.2%; Score 39; DB 15; Length 403;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 EFGAGLVGGQFM 13
Db      152 DVGAGLVGGDL 164
```

```

RESULT 10
; Sequence 41675, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41675
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-006-F6_FLI.pep
US-10-425-114-41675
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 11
US-10-425-114-48462
; Sequence 48462, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
```

```

; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48462
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-100-A6_FLI.pep
US-10-425-114-48462
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 12
US-10-425-114-49554
; Sequence 49554, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49554
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-213-B12_FLI.pep
US-10-425-114-49554
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 13
US-10-282-122A-50158
; Sequence 50158, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
```

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 50158
LENGTH: 419
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50158

Query Match 58.2%; Score 39; DB 14; Length 419;
Best Local Similarity 61.5%; Pred. No. 4.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQFM 13
DB 254 EFGAGLVGGQFM 266

RESULT 14
US-10-402-842-30
Sequence 30, Application US/10402842
Publication No. US20030219872A1
GENERAL INFORMATION:
APPLICANT: Magarvey, Nathan A.
APPLICANT: Hucul, John A.
TITLE OF INVENTION: NON-RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GEN
FILE REFERENCE: 0630/10854-US1
CURRENT APPLICATION NUMBER: US/10/402,842
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/368,713
PRIOR FILING DATE: 2002-03-30
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent version 3.1
SEQ ID NO 30
LENGTH: 450
TYPE: PRT
ORGANISM: Streptomyces hygroscopicus
US-10-402-842-30

Query Match 58.2%; Score 39; DB 14; Length 450;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAAGLVGGQF 12
DB 305 FGAAGLVGGQF 315

RESULT 15
US-10-369-493-21791
Sequence 21791, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21791
LENGTH: 528
TYPE: PRT
ORGANISM: Rhodobacter capsulatus
US-10-369-493-21791

Query Match 58.2%; Score 39; DB 14; Length 528;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQF 12
DB 263 EFGAGLVGGQF 274

RESULT 16
US-10-156-761-11459
Sequence 11459, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMTA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11459
LENGTH: 545
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-11459

Query Match 58.2%; Score 39; DB 14; Length 545;
Best Local Similarity 70.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGLVGGQFM 13
DB 332 AGLVGGQFM 341

RESULT 17
US-10-369-493-3245
Sequence 3245, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.

```

; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3245
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(748)
; OTHER INFORMATION: unsure at all Xaa locations
; US-10-369-493-3245

```

```

Query Match      58.2%; Score 39; DB 14; Length 748;
Best Local Similarity 70.0%; Pred. No. 8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      111 FSAGLVIGGK 120

```

```

RESULT 18
US-10-369-493-22168
; Sequence 22168, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22168
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-369-493-22168

```

```

Query Match      58.2%; Score 39; DB 14; Length 770;
Best Local Similarity 70.0%; Pred. No. 8.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      142 FSAGLVIGGK 151

```

```

RESULT 19
US-10-128-714-8235
; Sequence 8235, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengdi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshtkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

```

```

; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8235
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-8235

```

```

Query Match      58.2%; Score 39; DB 14; Length 810;
Best Local Similarity 70.0%; Pred. No. 8.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      148 FSAGLVIGGK 157

```

```

RESULT 20
US-10-128-714-3235
; Sequence 3235, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengdi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshtkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3235
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-3235

```

```

Query Match      58.2%; Score 39; DB 14; Length 811;
Best Local Similarity 70.0%; Pred. No. 8.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 FGAGLVIGGQ 11
        |||||:|:~|:|
Db      148 FSAGLVIGGK 157

```

```
RESULT 21
US-10-424-599-231652
; Sequence 231652, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231652
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51202C.1.pep
US-10-424-599-231652
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 15; Length 94;
Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVGGQF 12
DB 26 FGATLLGAGF 36
```

```
RESULT 22
US-10-425-115-365962
; Sequence 365962, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365962
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96923C.1.pep
US-10-425-115-365962
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 94;
Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 GAGLVGGQFM 13
DB 69 GSHLILGGEFL 79
```

```
RESULT 23
US-10-425-115-294011
; Sequence 294011, Application US/10425115
; Publication No. US20040214272A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 294011
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_31222C.1.pep
US-10-425-115-294011
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 102;
Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVGG 10
DB 93 FGAGIVRG 101
```

```
RESULT 24
US-10-369-493-2228
; Sequence 2228, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2228
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(146)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2228
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 14; Length 146;
Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVGGQ 11
DB 58 FGATLLAGQ 67
```

```
RESULT 25
US-10-425-115-227826
; Sequence 227826, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227826
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139373C.1.pep
US-10-425-115-227826

Query Match          56.7%; Score 38; DB 17; Length 182;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  EFGAGLVIGG 10
      |||:||||
Db      94  EFGSGQALGG 103

RESULT 26
US-10-437-963-203753
; Sequence 203753, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203753
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98906C.1.pep
US-10-437-963-203753

Query Match          56.7%; Score 38; DB 16; Length 238;
Best Local Similarity 70.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  EFGAGLVIGG 10
      |||:||||
Db      184  EFGSGQALGG 193

RESULT 27
US-10-425-114-46558
; Sequence 46558, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven B
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46558
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700352025_FLI.pep
US-10-425-114-46558

Query Match          56.7%; Score 38; DB 15; Length 241;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2  FGAGLVIGG 10
      |||:||||
Db      124  FGCGVILGG 132

RESULT 28
US-10-424-599-205502
; Sequence 205502, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205502
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27597C.1.pep
US-10-424-599-205502

Query Match          56.7%; Score 38; DB 15; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2  FGAGLVIGG 10
      |||:||||
Db      132  FGCGVILGG 140

RESULT 29
US-10-437-963-174772
; Sequence 174772, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174772

```


LENGTH: 249
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_72682C.1.pep
US-10-437-963-174772

Query Match
Best Local Similarity 56.7%; Score 38; DB 16; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 30
US-10-425-115-231962
Sequence 231962, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231962
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143142C.1.pep
US-10-425-115-231962

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 31
US-10-425-115-231963
Sequence 231963, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231963
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143143C.1.pep
US-10-425-115-231963

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 32
US-10-425-115-283162
Sequence 283162, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283162
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21341C.1.pep
US-10-425-115-283162

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 33
US-10-425-115-283165
Sequence 283165, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283165
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21344C.1.pep
US-10-425-115-283165

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 34
US-10-425-115-283167

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; Sequence 283167, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283167
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(249)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21346C.1.pcp
; US-10-425-115-283167
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```
Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
```

```
RESULT 35
US-10-425-115-283173
; Sequence 283173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283173
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21351C.1.pcp
; US-10-425-115-283173
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Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
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RESULT 36
US-10-425-115-284033
; Sequence 284033, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 284033
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_22138C.1.pcp
; US-10-425-115-284033
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Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
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RESULT 37
US-10-739-930-7930
; Sequence 7930, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7930
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAWA-23APR03-C3166_22.p
; US-10-739-930-7930
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Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
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RESULT 38
US-10-424-599-205503
; Sequence 205503, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205503
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Glycine max
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1256)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27598C.1.pep
US-10-424-599-205503

Query Match
Best Local Similarity 56.7%; Score 38; DB 15; Length 256;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVLCG 10
DB 139 FCGGVILCG 147

RESULT 39
US-10-437-963-174771
; Sequence 174771, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174771
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72681C.1.pep
US-10-437-963-174771

Query Match
Best Local Similarity 56.7%; Score 38; DB 16; Length 257;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVLCG 10
DB 140 FCGGVILCG 148

RESULT 40
US-10-425-114-41579
; Sequence 41579, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41579
; LENGTH: 259
; TYPE: PRT
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3078-037-G4_FLI.pep
US-10-425-114-41579

Query Match
Best Local Similarity 56.7%; Score 38; DB 15; Length 259;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVLCG 10
DB 142 FCGGVILCG 150

Search completed: December 9, 2004, 09:37:49
Job time : 5.58273 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 09:21:02 ; Search time 191.417 Seconds
(without alignments)
1013.220 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861

Sequence: 1 MVAVGALLAALAAFGAAL.....LILRSKPELQSSIRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1921	67.1	592	9	US-09-313-942-8
2	1921	67.1	592	9	US-09-313-942-8
3	1921	67.1	592	9	US-09-313-942-8
4	1921	67.1	592	9	US-09-313-942-8
5	1918	67.0	592	14	US-10-287-035-8
6	1918	67.0	592	14	US-10-287-035-8
7	1910	66.8	360	9	US-09-313-942-15
8	1910	66.8	360	9	US-09-313-942-15
9	1910	66.8	360	14	US-10-287-035-15
10	1823.5	63.7	360	14	US-10-282-162-15
11	1788	62.5	1158	9	US-10-322-696-144
12	1788	62.5	1158	9	US-09-313-942-26
13	1788	62.5	1158	14	US-10-287-035-26

14	1788	62.5	1158	14	US-10-282-162-26	Sequence 26, Appl
15	1783	62.3	1168	9	US-09-313-942-24	Sequence 24, Appl
16	1783	62.3	1168	9	US-09-313-942-24	Sequence 24, Appl
17	1783	62.3	1168	14	US-10-287-035-24	Sequence 24, Appl
18	1783	62.3	1168	14	US-10-282-162-24	Sequence 24, Appl
19	1683	58.8	315	9	US-09-313-942-16	Sequence 16, Appl
20	1683	58.8	315	9	US-09-313-942-16	Sequence 16, Appl
21	1683	58.8	315	14	US-10-287-035-16	Sequence 16, Appl
22	1683	58.8	315	14	US-10-282-162-16	Sequence 16, Appl
23	954.5	33.4	387	16	US-10-322-696-141	Sequence 14, Appl
24	954.5	33.4	460	14	US-10-247-463-13	Sequence 14, Appl
25	938.5	32.8	212	9	US-09-854-280-14	Sequence 14, Appl
26	938.5	32.8	212	9	US-09-854-280-14	Sequence 14, Appl
27	938.5	32.8	212	14	US-10-099-007A-3	Sequence 13, Appl
28	938.5	32.8	212	14	US-10-400-377-13	Sequence 13, Appl
29	938.5	32.8	212	14	US-10-400-708-13	Sequence 13, Appl
30	938.5	32.8	212	14	US-10-298-148-13	Sequence 13, Appl
31	938.5	32.8	212	15	US-10-440-464-61	Sequence 61, Appl
32	938.5	32.8	212	16	US-10-773-939-13	Sequence 13, Appl
33	938.5	32.8	212	16	US-10-773-939-13	Sequence 13, Appl
34	938.5	32.8	212	17	US-10-773-654-13	Sequence 13, Appl
35	938.5	32.8	212	17	US-10-828-343-3	Sequence 3, Appl
36	938.5	32.8	212	17	US-10-866-540-13	Sequence 13, Appl
37	938.5	32.8	212	17	US-10-276-642-6	Sequence 6, Appl
38	936.5	32.7	347	17	US-10-763-619-8	Sequence 8, Appl
39	935	32.7	317	14	US-10-083-446-145	Sequence 14, Appl
40	934	32.6	184	14	US-10-053-355A-3	Sequence 3, Appl
41	934	32.6	186	14	US-10-083-446-163	Sequence 163, Appl
42	930.5	32.5	212	9	US-09-908-594-14	Sequence 14, Appl
43	930.5	32.5	212	17	US-10-197-816-14	Sequence 14, Appl
44	930	32.5	207	15	US-10-264-049-3061	Sequence 3061, Ap
45	927	32.4	183	16	US-10-658-834A-198	Sequence 198, Ap

ALIGNMENTS

RESULT 1
US-09-313-942-8
Sequence 8, Application US/09313942
Publication No. US20020012962A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-09-313-942-8

Query Match 67.1%; Score 1921; DB 9; Length 592;
Best Local Similarity 77.1%; Pred. No. 3.7e-140;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;
QY 1 MVAVGALLAALAAFGAALAPRCPAEOVARCVLTSLPDSVTLTCCPGVEPDNATVHW 60
1 MVAVGALLAALAAFGAALAPRCPAEOVARCVLTSLPDSVTLTCCPGVEPDNATVHW 60
DB 61 VLRKPAAGSHPSWMAQGRRLILRSVQLHDSGVSCYRAGRPAQTHLLVDPVPEEPQLS 120
61 VLRKPAAGSHPSWMAQGRRLILRSVQLHDSGVSCYRAGRPAQTHLLVDPVPEEPQLS 120
QY 121 CFRKSPLSNVVCWBGSRTPSLTTKAVLVVRKQNSPADDFQRCQSOESQKFSQCLAV 180

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Db      121 CFFKSPLSNVVCEMGRSTPSLTTKAVLLVRKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Qy      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Db      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVO--- 357
Qy      361 VPPGDSKDVAAPRROPILTSSERIDKQIRYILDGISMARETKNSMCE--SSKEALAE 418
Db      358 -----DAGEP-----KSCDKHTTCCPCAPBELLGG 382
Qy      419 NNILNLPKRAEKDGCFOGFGNEETCLVKIIT---GLFEVYLEYLQ---NRPESSEBOAR 472
Db      383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNAKTKREROYN 442
Qy      473 AVQMSKTVL 481
Db      443 STYRVVSVL 451

```

RESULT 2

```

US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

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```

Query Match      67.1%; Score 1921; DB 9; Length 592;
Best Local Similarity 77.1%; Pred. No. 3,7e-140;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

```

```

Qy      1 MIAVGCALLAALIAAPGALAAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db      1 MIAVGCALLAALIAAPGALAAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCTYRAGRPAQTVHLLVDVPEEPQIS 120
Db      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCTYRAGRPAQTVHLLVDVPEEPQIS 120
Qy      121 CFFKSPLSNVVCEMGRSTPSLTTKAVLLVRKFQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Db      121 CFFKSPLSNVVCEMGRSTPSLTTKAVLLVRKFQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Qy      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Db      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

```

```

Db      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVO--- 357
Qy      361 VPPGDSKDVAAPRROPILTSSERIDKQIRYILDGISMARETKNSMCE--SSKEALAE 418
Db      358 -----DAGEP-----KSCDKHTTCCPCAPBELLGG 382
Qy      419 NNILNLPKRAEKDGCFOGFGNEETCLVKIIT---GLFEVYLEYLQ---NRPESSEBOAR 472
Db      383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNAKTKREROYN 442
Qy      473 AVQMSKTVL 481
Db      443 STYRVVSVL 451

```

RESULT 3

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US-10-287-035-8
; Sequence 8, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: AND USING
; CURRENT APPLICATION NUMBER: US/10/287,035
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-8

```

```

Query Match      67.1%; Score 1921; DB 14; Length 592;
Best Local Similarity 77.1%; Pred. No. 3,7e-140;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

```

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Qy      1 MIAVGCALLAALIAAPGALAAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db      1 MIAVGCALLAALIAAPGALAAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCTYRAGRPAQTVHLLVDVPEEPQIS 120
Db      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCTYRAGRPAQTVHLLVDVPEEPQIS 120
Qy      121 CFFKSPLSNVVCEMGRSTPSLTTKAVLLVRKFQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Db      121 CFFKSPLSNVVCEMGRSTPSLTTKAVLLVRKFQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRLSTWQD 240
Qy      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Db      241 PHSNNSFYRLRFELRYRARSKTFTTWVKDLOHHCVIDAMSGLRHVVQLRAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db      301 GEMSEMSPEAMGTPTWTSRSPPAENEYSTPMQALTTNKDDNILFRDSANATSLPVO--- 357

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Qy 361 VPEGDSKDVAAAPHROPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
 Db 358 -----DAGE-----KSCDKHTHTEPCPCAPPELLGG 382
 Qy 419 NNILNLPKMAKCGCFOSGNETCTLVKIIIT--GLLEFEVYLEYO--NREPSSEQAR 472
 Db 383 PSVFLPPEPKDQTLMTISRTPEVTCVVAVDSHEDPEVKFMVYDGVENAKTKFREEOQN 442
 Qy 473 AVQMSKVL 481
 Db 443 STYRVSVL 451

RESULT 4

US-10-282-162-8
 ; Sequence 8, Application US/10282162
 ; Publication No. US20030143697A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; TITLE OF INVENTION: AND USING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-282-162-8

Query Match 67.1%; Score 1921; DB 14; Length 592;

Best Local Similarity 77.1%; Pred. No. 3,7e-140; Indels 46; Gaps 5;
 Matches 377; Conservative 22; Mismatches 44;

Qy 1 MLAVGALLAALLAALPAAALPAPRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALLAALPAAALPAPRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHM 60
 Qy 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRPAQVHLLVDVPEEPOL 120
 Db 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRPAQVHLLVDVPEEPOL 120
 Qy 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFCQLAV 180
 Db 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFCQLAV 180
 Qy 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSVTWOD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSVTWOD 240
 Qy 241 PHSWNSFFYRLRFLRYRARSKTFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Db 241 PHSWNSFFYRLRFLRYRARSKTFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Qy 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Db 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Qy 361 VPEGDSKDVAAAPHROPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
 Db 358 -----DAGE-----KSCDKHTHTEPCPCAPPELLGG 382
 Qy 419 NNILNLPKMAKCGCFOSGNETCTLVKIIIT--GLLEFEVYLEYO--NREPSSEQAR 472
 Db 383 PSVFLPPEPKDQTLMTISRTPEVTCVVAVDSHEDPEVKFMVYDGVENAKTKFREEOQN 442
 Qy 473 AVQMSKVL 481

Db 443 STYRVSVL 451

RESULT 5

US-10-247-463-12
 ; Sequence 12, Application US/10247463
 ; Publication No. US20030082734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dowling, Lynette M.
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Kastelein, Robert A.
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: DX09920
 ; CURRENT APPLICATION NUMBER: US/10/247,463
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US/09/588,113
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 468
 ; TYPE: PRT
 ; ORGANISM: primate
 US-10-247-463-12

Query Match 67.0%; Score 1918; DB 14; Length 468;

Best Local Similarity 96.5%; Pred. No. 4.6e-140; Indels 8; Gaps 1;
 Matches 360; Conservative 1; Mismatches 4;

Qy 1 MLAVGALLAALLAALPAAALPAPRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALLAALPAAALPAPRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHM 60
 Qy 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRPAQVHLLVDVPEEPOL 120
 Db 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRPAQVHLLVDVPEEPOL 120
 Qy 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFCQLAV 180
 Db 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFCQLAV 180
 Qy 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSVTWOD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSVTWOD 240
 Qy 241 PHSWNSFFYRLRFLRYRARSKTFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Db 241 PHSWNSFFYRLRFLRYRARSKTFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Qy 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Db 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Qy 361 VPEGDSKDVAAAPHROPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
 Db 357 ----ODSSSVPLP 365

RESULT 6

US-09-313-942-15
 ; Sequence 15, Application US/09313942
 ; Publication No. US20020012962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; CURRENT FILING DATE: 1999-05-19

;; PRIOR APPLICATION NUMBER: 09/313,942
;; PRIOR FILING DATE: 1999-05-19
;; PRIOR APPLICATION NUMBER: 60/101,858
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 15
;; LENGTH: 360
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 9; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357

RESULT 7
US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match 66.8%; Score 1910; DB 9; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357

RESULT 8
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match 66.8%; Score 1910; DB 14; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCGVEPEDNATVHM 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNYSCYRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQYQSQSKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVANPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYARERSKFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357


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RESULT 9
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-282-162-15

```

Query Match	66.8%	Score 1910;	DB 14	Length 360;
Best Local Similarly	99.4%	Pred. No. 1.3e-139;		
Matches 355;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	MLAVGALLAALLAAAGALLAARRCAQAVAGVLTSLPGDSVTLTCGVEPENAATVW	60
Qy	1	
Db	MVAVGALLAALLAAAGALLAARRCAQAVAGVLTSLPGDSVTLTCGVEPENAATVW	60
Qy	61	
Db	VLKRPAGSHPSRMAGKRRLLRLSYQLHDSNGSYCYAGRAGTWHLLVDPPEEPOLS	120
Qy	61	
Db	VLKRPAGSHPSRMAGKRRLLRLSYQLHDSNGSYCYAGRAGTWHLLVDPPEEPOLS	120
Qy	121	
Db	CFKPSPLSNVNCWCGRSTPSLTLTKVLLVYRKFNQSPADPFQPCQSQSKSCQALV	180
Qy	121	
Db	CFKPSPLSNVNCWCGRSTPSLTLTKVLLVYRKFNQSPADPFQPCQSQSKSCQALV	180
Qy	181	
Db	PEQDSSFYLYSMCVASSVSGSKPSKSTQTFQCGGILLDRPPRANTTVAANRPMILSVTWQD	240
Qy	181	
Db	PEQDSSFYLYSMCVASSVSGSKPSKSTQTFQCGGILLDRPPRANTTVAANRPMILSVTWQD	240
Qy	241	
Db	PHSMNSFYRLRELYRAERASKTPTTMMVKDLQHNHCYIHDMSGRLRYVQLRAQEEFGQ	300
Qy	241	
Db	PHSMNSFYRLRELYRAERASKTPTTMMVKDLQHNHCYIHDMSGRLRYVQLRAQEEFGQ	300
Qy	301	
Db	GEVSEVSPKMGTPWTEESRSPRAENEVSITPMQALLTNKDDNILLRDSANNTSLPVE	357
Qy	301	
Db	GEVSEVSPKMGTPWTEESRSPRAENEVSITPMQALLTNKDDNILLRDSANNTSLPVE	357

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RESULT 10
US-10-322-696-144
: Sequence 144, Application US/10322696
: Publication No. US20040166490A1
: GENERAL INFORMATION:
: APPLICANT: MOTTIS, David W.
: APPLICANT: Malandino, Marc
: TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
: FILE REFERENCE: 529452001300
: CURRENT APPLICATION NUMBER: US/10/322,696
: CURRENT FILING DATE: 2003-10-17
: NUMBER OF SEQ. ID NOS: 186
: SOFTWARE: PasteSeq for Windows Version 4.0
: SEQ. ID NO. 144
: LENGTH: 453
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-322-696-144

```

Query Match	63.7%	Score 1823.5	DB 16	Length 453
Best Local Similarity	92.5%	Pred. No. 9.4e-133		
Matches 345	Conservative 1	Mismatches 4	Indels 23	Gaps 2

```

QY      1  MLAGCMLAALLAALPAAGAAAPRRCPAQEVARGVLTSLPGDSVTLTCQVEEEDNATVHM  60
Db      1  MLAGCMLAALLAALPAAGAAAPRRCPAQEVARGVLTSLPGDSVTLTCQVEEEDNATVHM  60

QY      61  VLRRPAAGSHPSRWAGMGRLLLSVOLHDSGNTSYRAGRPAGTVHLLDVVPPEPOL  120
Db      61  VLRRPAAGSHPSRWAGMGRLLLSVOLHDSGNTSYRAGRPAGTVHLLDVVPPEPOL  120

QY      121  CFRKSPLSNVTCQEWGPRSTPSLTTKAVLLYRKQNSPAEDPQEPQYQSQSQKFSQQLAV  180
Db      121  CFRKSPLSNVTCQEWGPRSTPSLTTKAVLLYRKQNSPAEDPQEPQYQSQSQKFSQQLAV  180

QY      181  PEGRSSFYIVMCAVSSVGSKFSTQTFQCGCIILOPDPANITTVAAVARNPMLSVTWOD  240
Db      181  PEGRSSFYIVMCAVSSVGSKFSTQTFQCGCIILOPDPANITTVAAVARNPMLSVTWOD  240

QY      241  PHSNMSSEFYRLRFELRYRBAERSKTFTTMVYDLOHHCYIHDMSGLRHVYVOLAQEEFQ  300
Db      241  PHSNMSSEFYRLRFELRYRBAERSKTFTTMVYDLOHHCYIHDMSGLRHVYVOLAQEEFQ  300

QY      301  GEMSEWSEPMANGTPTWTSRSPPAENENSTPMQALTTNKDDNII LRDSANATSLPVEFMP  360
Db      301  GEMSEWSEPMANGTPTWTE-----ALTTNKDDNII LRDSANATSLPV-----  341

QY      361  VPPGEDSKDVAAAP  373
Db      342  ----QDSSVPLP  350

```

```

RESULT 11
US-09-313-942-26
Sequence 26, Application US/09313942
Publication No. US20020012962A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 26
LENGTH: 1158
TYPE: PRT
ORGANISM: Homo sapiens
US-09-313-942-26

```

Query Match	62.5%	Score 1788	DB 9	Length 1158
Best Local Similarity	99.1%	Pred. No. 2e-129		
Matches 331	Conservative 2	Mismatches 1	Indels 0	Gaps 0
QY	1	MLAVGALLAALLAAPGATAAPRCPCPADEVARGVLTSLPGDSVTLLTCGVEBEDNATVHM	60	
	:			
Db	1	MVAVGALLAALLAAPGALLAPRCPCPADEVARGVLTSLPGDSVTLLTCGVEBEDNATVHM	60	
QY	61	VLRRPAGSHSRNAGGRLLRLRSVQHDGNGNSCYRAGRPAGVHLLLVNVPPEPOLS	120	
	:			
Db	61	VLRRPAGSHSRNAGGRLLRLRSVQHDGNGNSCYRAGRPAGVHLLLVNVPPEPOLS	120	
QY	121	CFRRSPLSNVNCEWGPRTSPSLITTKAVLIVKFNQNSPAEDRQEBQCYQESQKSCQLAV	180	
	:			
Db	121	CFRRSPLSNVNCEWGPRTSPSLITTKAVLIVKFNQNSPAEDRQEBQCYQESQKSCQLAV	180	
QY	181	PEGDSFFIYVMCAVSSVGSKFSKSTQTFQGCGLIQDPDPANITVTYVARNPMLSVTMMOD	240	

QY 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 Db 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 QY 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 Db 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 QY 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 Db 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 Db 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 334
 Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 334

RESULT 15

US-09-313-942-24
 ; Sequence 24, Application US/09313942
 ; Publication No. US20020012962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 1168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-313-942-24

Query Match 62.3%; Score 1783; DB 9; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 4,9e-129;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 Db 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 QY 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 Db 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 QY 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 Db 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 Db 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 331

Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 331

RESULT 16

US-09-935-868-24
 ; Sequence 24, Application US/09935868
 ; Patent No. US20020164690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Regeneron Pharmaceuticals, Inc
 ; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
 ; FILE REFERENCE: REG 203D
 ; CURRENT APPLICATION NUMBER: US/09/935,868
 ; PRIOR FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 1168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-935-868-24

Query Match 62.3%; Score 1783; DB 9; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 4,9e-129;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALAAAGALAPRRCPAEOVARGVLTSLPGDSVTLTTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 Db 61 VLRKPAAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPQOLS 120
 QY 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 Db 121 CPEKSPLSNVVCEWGRSTPSLTTKAVLVRKQNSPAEDFOEPCQYSQESQKFSQOLAV 180
 QY 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 Db 181 PEDGSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 Db 241 PHSWNSFFYRLRELRYRARSKTFTTMVKDLOHHCVIHDAMSGLRHVVLRAQEEFQ 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 331
 Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPM 331

RESULT 17

US-10-287-035-24
 ; Sequence 24, Application US/10287035
 ; Publication No. US20030104567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neil Stahl and George D. Yancopoulos
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203DA
 ; CURRENT APPLICATION NUMBER: US/10/287,035
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: USSN 09/935,868
 ; PRIOR FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: USSN 09/787,835
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: USSN 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 24
 LENGTH: 1168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-287-035-24

Query Match 62.3%; Score 1783; DB 14; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 4,9e-129;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 DB 1 MVAAGCALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 QY 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120
 DB 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 QY 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 DB 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 QY 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPM 331
 DB 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPM 331

RESULT 18
 US-10-282-162-24
 Sequence 24, Application US/10282162
 Publication No. US20030143697A1
 GENERAL INFORMATION:
 APPLICANT: REGENERON PHARMACEUTICALS, INC.
 TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 FILE REFERENCE: REG 203-B-US
 CURRENT FILING DATE: 2002-10-28
 CURRENT APPLICATION NUMBER: 09/787,835
 PRIOR FILING DATE: 1999-09-22
 PRIOR APPLICATION NUMBER: PCT/US99/22045
 PRIOR FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 24
 LENGTH: 1168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-282-162-24

Query Match 62.3%; Score 1783; DB 14; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 4,9e-129;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 DB 1 MVAAGCALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 QY 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120
 DB 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120

QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 QY 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 DB 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 QY 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPM 331
 DB 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPM 331

RESULT 19
 US-09-313-942-16
 Sequence 16, Application US/09313942
 Publication No. US20020012962A1
 GENERAL INFORMATION:
 APPLICANT: REGENERON PHARMACEUTICALS, INC.
 TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 FILE REFERENCE: REG 203-A
 CURRENT FILING DATE: 1999-05-19
 CURRENT APPLICATION NUMBER: 09/313,942
 PRIOR FILING DATE: 1999-05-19
 PRIOR APPLICATION NUMBER: 60/101,856
 PRIOR FILING DATE: 1998-09-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 16
 LENGTH: 315
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-313-942-16

Query Match 58.8%; Score 1683; DB 9; Length 315;
 Best Local Similarity 99.7%; Pred. No. 4,5e-122;
 Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 DB 1 MVAAGCALLAALAAAPGALAPRCPOEVARAGVLTSLPGDSVTLLTCGVEPEDNATVHW 60
 QY 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120
 DB 61 VLKRPAGSHPSRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLLVRFKQNSPAEDFOEPCQYSQESQKSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVAVANRPMWLSVTWOD 240
 QY 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 DB 241 PHSWNSFFYRLRFEELRYRAERSKTFTTMVVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 QY 301 GEMSEMSPEAMGT 313
 DB 301 GEMSEMSPEAMGT 313

RESULT 20
 US-09-935-868-16
 Sequence 16, Application US/09935868
 Patent No. US20020164690A1

GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-868-16

Query Match 58.8%; Score 1683; DB 9; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
DB 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
QY 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
DB 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
QY 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||
DB 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||
QY 241 PHSWNSFFYRLRPELRRAERSKFTTMMVKDLOHHCIVHDAMSGLRHVQLRAQBEFQ 300
|:|||||
DB 241 PHSWNSFFYRLRPELRRAERSKFTTMMVKDLOHHCIVHDAMSGLRHVQLRAQBEFQ 300
|:|||||
QY 301 GEMSEWSPAMGT 313
|:|||||
DB 301 GEMSEWSPAMGT 313
|:|||||

RESULT 21
US-10-287-035-16
Sequence 16, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-035-16

Query Match 58.8%; Score 1683; DB 14; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
DB 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
QY 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
DB 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
QY 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||
DB 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||
QY 241 PHSWNSFFYRLRPELRRAERSKFTTMMVKDLOHHCIVHDAMSGLRHVQLRAQBEFQ 300
|:|||||
DB 241 PHSWNSFFYRLRPELRRAERSKFTTMMVKDLOHHCIVHDAMSGLRHVQLRAQBEFQ 300
|:|||||
QY 301 GEMSEWSPAMGT 313
|:|||||
DB 301 GEMSEWSPAMGT 313
|:|||||

RESULT 22
US-10-282-162-16
Sequence 16, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-162-16

Query Match 58.8%; Score 1683; DB 14; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
DB 1 MVAVGALLAALAAAGALAPRRCPAQBVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
|:|||||
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
|:|||||
QY 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
DB 121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFQNSPADPFOBPQCYSGESQKFSQCLAV 180
|:|||||
QY 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||
DB 181 PGDSSFFIYVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
|:|||||

QY 241 PHSWNSFYRLRELAAYRABRSKFTTMMVKDLOHHCYIHDAMSGLRHVQVLAQOEFG 300
 DB 241 PHSWNSFYRLRELAAYRABRSKFTTMMVKDLOHHCYIHDAMSGLRHVQVLAQOEFG 300
 QY 301 GEMSEWSPAMGT 313
 DB 301 GEMSEWSPAMGT 313

RESULT 23

US-10-322-696-141
 ; Sequence 141, Application US/10322696
 ; Publication No. US20040166490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Malandro, Marc
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
 ; FILE REFERENCE: 529452001200
 ; CURRENT APPLICATION NUMBER: US/10/322,696
 ; CURRENT FILING DATE: 2003-10-17
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 141
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-322-696-141

Query Match 33.4%; Score 954.5; DB 16; Length 387;
 Best Local Similarity 50.1%; Pred. No. 2e-65;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MIAVGCALLAALLAAPGALLAPRCPAQEVARGVLTSLPGDSVYTLTCGVEPEDNATVHM 60
 DB 2 MLTVGCTLLVALLAPVALVIGSCRALEVANGVTSLPGATVTLICPKKAAGNVITIM 61
 QY 61 VLRKAAGSHPSRMAGMGRRLILRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
 DB 62 VY----SSQNRKEMTTGNTLVLDVQSLDYGILCSLNDHLVGTVPVLDVPEEPQLS 117
 QY 121 CERKSPLSNVVCEWGPSTPSLTTRKAVLVKRFQNSPAE-DFOEPCCYQSQSKSCOLA 179
 DB 118 CRRKNPLVNAICEMWRSPSTPTTKAVLPAKKINTNGKSDFOVPCQYSQLKSFSCQVE 177
 QY 180 VPEGDSFPIYVMCAVSSVGSFKSTQTFQCGILQPPDPANITVTAARNPMLSVTWQ 239
 DB 178 ILGDKVYHIVSLCVANSVGSKSHNEAFHSLKMOVDPDPANLVVSAIGRRMLKYSWQ 237
 QY 240 DPHSWNSFYRLRELAAYRABRSKFTTMMVKDLOHHCYIHDAMSGLRHVQVLAQOEFG 299
 DB 238 HPEWTDSYLLQPOLRYRPMWSKEFTVLLPVAQYQCVIHDALRGVHVVQVKGKEILD 297
 QY 300 QGEMSEWSPAMGTPW-TESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPYEF 358
 DB 298 LGQSEWSPVETGTPWIAEPRITPA-GILMNPQVSDSANHDEQYSSSTATSV---- 352
 QY 359 MPVPGEDESKDVAA 373
 DB 353 --LAPVOESSMSLP 365

RESULT 24

US-10-247-463-13
 ; Sequence 13, Application US/10247463
 ; Publication No. US20030082734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dowling, Lynette M.
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Kastelein, Robert A.
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
 ; TITLE OF INVENTION: Methods

FILE REFERENCE: DX09920
 ; CURRENT APPLICATION NUMBER: US/10/247,463
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US/09/588,113
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: rodent
 US-10-247-463-13

Query Match 33.4%; Score 954.5; DB 14; Length 460;
 Best Local Similarity 50.1%; Pred. No. 2.6e-65;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MIAVGCALLAALLAAPGALLAPRCPAQEVARGVLTSLPGDSVYTLTCGVEPEDNATVHM 60
 DB 1 MLTVGCTLLVALLAPVALVIGSCRALEVANGVTSLPGATVTLICPKKAAGNVITIM 60
 QY 61 VLRKAAGSHPSRMAGMGRRLILRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
 DB 61 VY----SSQNRKEMTTGNTLVLDVQSLDYGILCSLNDHLVGTVPVLDVPEEPQLS 116
 QY 121 CERKSPLSNVVCEWGPSTPSLTTRKAVLVKRFQNSPAE-DFOEPCCYQSQSKSCOLA 179
 DB 117 CRRKNPLVNAICEMWRSPSTPTTKAVLPAKKINTNGKSDFOVPCQYSQLKSFSCQVE 176
 QY 180 VPEGDSFPIYVMCAVSSVGSFKSTQTFQCGILQPPDPANITVTAARNPMLSVTWQ 239
 DB 177 ILGDKVYHIVSLCVANSVGSKSHNEAFHSLKMOVDPDPANLVVSAIGRRMLKYSWQ 236
 QY 240 DPHSWNSFYRLRELAAYRABRSKFTTMMVKDLOHHCYIHDAMSGLRHVQVLAQOEFG 299
 DB 237 HPEWTDSYLLQPOLRYRPMWSKEFTVLLPVAQYQCVIHDALRGVHVVQVKGKEILD 296
 QY 300 QGEMSEWSPAMGTPW-TESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPYEF 358
 DB 297 LGQSEWSPVETGTPWIAEPRITPA-GILMNPQVSDSANHDEQYSSSTATSV---- 351
 QY 359 MPVPGEDESKDVAA 373
 DB 352 --LAPVOESSMSLP 364

RESULT 25

US-09-854-280-14
 ; Sequence 14, Application US/09854280
 ; Patent No. US20020052027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C2
 ; CURRENT APPLICATION NUMBER: US/09/854,280
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/085,579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: US 60/113,621
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 14
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-280-14

Query Match 32.8%; Score 938.5; DB 9; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPEVF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 81

QY 413 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 26
US-09-854-208-14
; Sequence 14, Application US/09854208
; Patent No. US20020106743A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jjian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
; FILE REFERENCE: P1381-R1
; CURRENT APPLICATION NUMBER: US/09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US/09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-208-14

Query Match 32.8%; Score 938.5; DB 9; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPEVF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 81

QY 413 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 27

US-10-099-007A-3
; Sequence 3, Application US/10099007A
; Publication No. US20030017150A1
; GENERAL INFORMATION:
; APPLICANT: Theodore Torphy
; TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED IMMUNOGLOBULIN
; FILE REFERENCE: CEN-0266
; DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; CURRENT APPLICATION NUMBER: US/10/099,007A
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-007A-3

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPEVF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 81

QY 413 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKKNDIAITTPDPTTNASLITKLOAQNOMLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 28
US-10-400-377-13
; Sequence 13, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-13

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPEVF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNCESS 81

QY 413 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFCGSENEETCLVKIITGLLEFEVYLYLQNRFFSSSEQAR 141

```
QY 473 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 532
      |||
Db 142 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 201
      |||
QY 533 LOSSLRALROM 543
      |||
Db 202 LOSSLRALROM 212

RESULT 29
US-10-400-708-13
; Sequence 13, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-400-708-13

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      |||
Db 22 LPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
      |||
QY 413 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      |||
Db 82 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
      |||
QY 473 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 532
      |||
Db 142 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 201
      |||
QY 533 LOSSLRALROM 543
      |||
Db 202 LOSSLRALROM 212

RESULT 30
US-10-298-148-13
; Sequence 13, Application US/10298148
; Publication No. US20030171264A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
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; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-298-148-13

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      |||
Db 22 LPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
      |||
QY 413 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      |||
Db 82 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
      |||
QY 473 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 532
      |||
Db 142 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 201
      |||
QY 533 LOSSLRALROM 543
      |||
Db 202 LOSSLRALROM 212

RESULT 31
US-10-440-464-61
; Sequence 61, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, AYESA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: AND ACTIVITY IN MAMMALS
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 212
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-440-464-61

Query Match 32.8%; Score 938.5; DB 15; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      |||
Db 22 LPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
      |||
QY 413 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      |||
Db 82 KEALAENNINLPKMAEKDGCFOGSEFNEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
      |||
QY 473 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 532
      |||
Db 142 AVQNSTKVLIOFLOKAKNLDATITPPPTNASLITKLOAQONWLODMTHLILRSFKEF 201
      |||
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QY	533	LOSSLRALRQM	543
Db	202	LOSSLRALRQM	212

RESULT 32
US-10-773-939-13

```

? Sequence 13 Application US/1077939
? Publication No. US20040175356A1
? GENERAL INFORMATION:
? APPLICANT: Cox III, George N
? APPLICANT: Bolder Biotechnology, Inc.
? TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
? FILE REFERENCE: 4152-1-PUS
? CURRENT APPLICATION NUMBER: US/10/773,939
? CURRENT FILING DATE: 2004-02-05
? PRIOR APPLICATION NUMBER: US/10/400,377
? PRIOR FILING DATE: 2003-03-26
? PRIOR APPLICATION NUMBER: US/09/462,941
? PRIOR FILING DATE: 2000-01-14
? PRIOR APPLICATION NUMBER: 60/052,516
? PRIOR FILING DATE: 1997-07-14
? NUMBER OF SEQ ID NOS: 41
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 13
? LENGTH: 212
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-773-939-13

```

Query Match	32.8%	Score 938.5;	DB 16;	Length 212;
Best Local Similarity	97.9%	Pred. No. 1.5e-64;		
Matches 187; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1;

Qy	354	LPPEF-MVPPEGSDSDVAAPHROPLTSSERIDKOIRYILGJISALRRETCNSMCESS	4122
Db	22	LPAPAPVPPEGSDSDVAAPHROPLTSSERIDKOIRYILGJISALRRETCNSMCESS	81
Qy	413	KEALAENNINLPRMAEKDCFSOGFNEETCLVKIITGLLEFEVYLEYLONRFBSSSEQAR	4722
Db	82	KEALAENNINLPRMAEKDCFSOGFNEETCLVKIITGLLEFEVYLEYLONRFBSSSEQAR	141
Qy	473	AVOMSTKVLIOFLQKKAKNLDAITTPDPPTNNSLLTKLOAONOMLOMTTHLIRSKFEF	5322
Db	142	AVOMSTKVLIOFLQKKAKNLDAITTPDPPTNNSLLTKLOAONOMLOMTTHLIRSKFEF	201
Qy	533	LOSSLRALROM	543
Db	202	LOSSLRALROM	212

RESULT 33
US-10-774-149-13

```

1 Sequence 13, Application US/10774149
2 Publication No. US20040175800A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Cox III, George N
7 APPLICANT: Boldor Biotechnology, Inc.
8
9 TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
10
11 FILE REFERENCE: 4152-1-PUS
12
13 CURRENT APPLICATION NUMBER: US/10/774,149
14
15 CURRENT FILING DATE: 2004-02-05
16
17 PRIOR APPLICATION NUMBER: US/10/400,377
18
19 PRIOR FILING DATE: 2003-03-26
20
21 PRIOR APPLICATION NUMBER: US/09/462,941
22
23 PRIOR FILING DATE: 2000-01-14
24
25 PRIOR APPLICATION NUMBER: 60/052,516
26
27 PRIOR FILING DATE: 1997-07-14
28
29 NUMBER OF SEQ ID NOS: 41
30
31 SOFTWARE: PatentIn Ver. 2.0
32
33 SEQ ID NO 13
34
35 LENGTH: 212
36
37 TYPE: PRT

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ORGANISM: Homo sapiens
US-10-774-149-13

Query Match	32.8%	Score 938.5;	DB 16;	Length 212;
Best Local Similarity	97.9%	Pred. No. 1.5e-64;		
Matches 187; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1.

Qy	413	KEALAENNINLPRMAEKDGFOSGNEETCLVKIITIGLLEFEVYLEYONRFESSEBOAR	472
Db	82	KEALAENNINLPRMAEKDGFOSGNEETCLVKIITIGLLEFEVYLEYONRFESSEBOAR	141
Qy	473	AVOMSTKVLIOFLOKKAKRLDAITTPDPTYNASILLTGLQAOONOLQDMTHILIRSKEF	532
Db	142	AVOMSTKVLIOFLOKKAKRLDAITTPDPTYNASILLTGLQAOONOLQDMTHILIRSKEF	201
Qy	533	LOSSLBALROM	543
Db	202	LOSSLBALROM	212

RESULT 34
US-10-773-654-13

```

Sequence 13, Application US/10773654
Publication No. US20040214287A1
GENERAL INFORMATION:
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/773,654
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-10-773-654-13

```

Query Match	32.8%	Score 938.5;	DB 17;	Length 212;
Best Local Similarity	97.9%	Pred. No. 1.5e-64;		
Matches 187; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1

Qy	35	LPPEF-MPPPEDSDUDVAAPHROGLTSSERIDQIRIILDGISALKEKCNKSNMCESS	412
Db	22	LPAPFAFPAPPPGEDSDUDVAAPHROPLTSSERIDQIRIILDGISALKEKCNKSNMCESS	81
Qy	413	KEALAENNINLPRMAEKDGCFOSGNEBETCLVKIITGLLEFEVYLEYLONRPESSSEBOAR	472
Db	82	KEALAENNINLPRMAEKDGCFOSGNEBETCLVKIITGLLEFEVYLEYLONRPESSSEBOAR	141
Qy	473	AVOMSTKVLIOFLQKKAKNLDAITTPDPTNVALITKLQAOQOMLODMTHLIRSRKEF	532
Db	142	AVOMSTKVLIOFLQKKAKNLDAITTPDPTNVALITKLQAOQOMLODMTHLIRSRKEF	201
Qy	533	LOSSLRALROM 543	
Db	202	LOSSLRALROM 212	

RESULT 35
US-10-828-343-3
; Sequence 3, Application US/10828343

```
; Publication No. US2004022838A1
; GENERAL INFORMATION:
; APPLICANT: FLECKENSTEIN, Bernhard
; NEIPEL, Frank
; FRIEDMAN-KIEN, Alvin
; HUANG, Yao-Qi
; TITLE OF INVENTION: VIRAL INTERLEUKIN-6
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/828,343
; FILING DATE: 21-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/230,048
; FILING DATE: 12-Mar-1999
; APPLICATION NUMBER: WO PCT/EP96/03199
; FILING DATE: 19-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 058315/0129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-828-343-3
Query Match          32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 354 LPVEF-MPVPGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAPFAPVPBGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYIQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYIQNRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITLQAOQONQLODMTTHILRSFKEF 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITLQAOQONQLODMTTHILRSFKEF 201
QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212
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RESULT 36
US-10-866-540-13
; Sequence 13, Application US/10866540
; Publication No. US20040230040A1
; GENERAL INFORMATION:
```

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; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/866,540
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-866-540-13
Query Match          32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 354 LPVEF-MPVPGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAPFAPVPBGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYIQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYIQNRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITLQAOQONQLODMTTHILRSFKEF 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITLQAOQONQLODMTTHILRSFKEF 201
QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212
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RESULT 37
US-10-276-642-6
; Sequence 6, Application US/10276642
; Publication No. US2004023156A1
; GENERAL INFORMATION:
; APPLICANT: Ralph, Stephen John
; TITLE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
; FILE REFERENCE: DAVI200.001APC
; CURRENT APPLICATION NUMBER: US/10/276,642
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PCT/AU01/00565
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: PQ 7553
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-642-6
Query Match          32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 354 LPVEF-MPVPGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAPFAPVPBGEDSKVAAAPHROPVTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYIQNRFSSSEQAR 472
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DB 82 KEALAEENLNLPMAEKDCFGSGFNEETCLVLIITGLLEFEVYLEYLQNRFFESSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMTHLILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMTHLILRSFKER 201
QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 38
US-10-763-619-8
; Sequence 8, Application US/10763619
; Publication No. US20040215008A1
; GENERAL INFORMATION:
; APPLICANT: Biochemie Gesellschaft m.b.H.
; TITLE OF INVENTION: Production of proteins
; FILE REFERENCE: G-31109/A/BCK
; CURRENT APPLICATION NUMBER: US/10/763,619
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 347
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligo-nucleotide purification aid combined with
; OTHER INFORMATION: sequences of Pestivirus and Homo sapiens
US-10-763-619-8

Query Match 32.7%; Score 936.5; DB 17; Length 347;
Best Local Similarity 94.9%; Pred. No. 4,4e-64;
Matches 187; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 350 NATSLPV---EFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 406
DB 151 NPTNCDLWMTSCAPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 210
QY 407 NNCCESSKEALAEENLNLPMAEKDCFGSGFNEETCLVLIITGLLEFEVYLEYLQNRFFES 466
DB 211 NNCCESSKEALAEENLNLPMAEKDCFGSGFNEETCLVLIITGLLEFEVYLEYLQNRFFES 270
QY 467 SEEOARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMTHLIL 526
DB 271 SEEOARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMTHLIL 330
QY 527 RSFKERLOSSLRALROM 543
DB 331 RSFKERLOSSLRALROM 347

RESULT 39
US-10-083-446-145
; Sequence 145, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Maite H.
; Eason, Alan M.
; Klein, Barbara K.
; McKeown, John P.
; Oline, Peter O.
; Paik, Kumman
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-9452
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-083-446-145

Query Match 32.7%; Score 935; DB 14; Length 317;
Best Local Similarity 63.0%; Pred. No. 5e-64;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;

QY 240 DPHSNNSFYRLRFEIRYARSKRTFTTMVYKDLQ-----HCVIDAMSGLR 287
DB 24 DPHNNSBMDIMERNLRTPNILAFVR-AVHGLENAIGIEILRLNLOCLPSATAAPSR 82
QY 288 HVYQLRAQBEFGGSEMS-----PEAMGTPT-ESRSPAEVSTPMQALTT 336
DB 83 HPIITIA-----GDMQREKLTFLVTLBOHQEQVIEGRISFGG----- 125
QY 337 NKDDNILFRDSANATSLPEFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIS 396
DB 126 -----SGGGSNM-----APVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIS 170
QY 397 ALRKETCNKSNNCCESSKEALAEENLNLPMAEKDCFGSGFNEETCLVLIITGLLEFEVY 456
DB 171 ALRKETCNKSNNCCESSKEALAEENLNLPMAEKDCFGSGFNEETCLVLIITGLLEFEVY 230
QY 457 LEYLQNRFFESSEEOARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQW 516
DB 231 LEYLQNRFFESSEEOARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQW 290
QY 517 LODMTTHLILRSFKERLOSSLRALROM 543
DB 291 LODMTTHLILRSFKERLOSSLRALROM 317

RESULT 40
US-10-053-355A-3
; Sequence 3, Application US/10053355A
; Publication No. US2003007824A1

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; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High Th
; TITLE OF INVENTION: Small Molecule Drug Discovery
; FILE REFERENCE: A-70982/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/053,355A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/316,723
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: patentin version 3.1
; SEQ ID NO 3
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-053-355A-3

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Query Match          32.6%; Score 934; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.8e-64; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

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QY      360  PVPFGEDSKDVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESSKEALAE 419
          |||||||
DB      1    PVPFGEDSKDVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESSKEALAE 60
          |||||||
QY      420  NNLPMGAEKDGCFQSGFNEETCLVKITITGLLEFEVYLEYLNRFESSEEQARAVQWSTK 479
          |||||||
DB      61  NNLPMGAEKDGCFQSGFNEETCLVKITITGLLEFEVYLEYLNRFESSEEQARAVQWSTK 120
          |||||||
QY      480  VLIQFQKAKNLDATITPPTTNASILTKLOAONQWLQDMTTHILRSFKEPQSSIRA 539
          |||||||
DB      121  VLIQFQKAKNLDATITPPTTNASILTKLOAONQWLQDMTTHILRSFKEPQSSIRA 180
          |||||||
QY      540  LROM 543
          |||
DB      181  LROM 184

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Search completed: December 9, 2004, 09:37:51
 Job time : 193.417 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:40:41 ; Search time 5.96223 Seconds
(without alignments)
1234.342 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVGQGM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	68.7	382	2 Q8U787	Q8U787 agrobacteri
2	46	68.7	402	2 Q7CVA1	Q7CVA1 agrobacteri
3	46	68.7	1171	1 N1RY_KLEPN	P03933 klebsiella
4	42	62.7	160	2 Q755M3	Q755M3 ashyia goss
5	42	62.7	160	2 AAS53165	AAS53165 ashbya go
6	42	62.7	396	2 Q9R823	Q9R823 deinococcus
7	42	62.7	540	2 Q6CC56	Q6CC56 yarowia ii
8	41	61.2	155	2 Q92P15	Q92P15 rhizobium m
9	41	61.2	291	2 Q84633	Q84633 chlamydia t
10	41	61.2	313	1 ATRX_YEAST	Q12067 saccharomyc
11	41	61.2	313	2 AAS53633	AAS53633 saccharomyc
12	41	61.2	319	2 Q82N27	Q82N27 streptomyces
13	41	61.2	331	2 Q6FMS6	Q6FMS6 candida gla
14	41	61.2	347	2 Q91G68	Q91G68 pseudomonas
15	41	61.2	444	2 Q74EW6	Q74EW6 geobacter b
16	41	61.2	444	2 AAR34173	AAR34173 geobacter
17	41	61.2	623	1 YFE9_YEAST	P43554 saccharomyc
18	41	61.2	765	2 Q6FPT7	Q6FPT7 candida gla
19	41	61.2	920	1 MML7_MYCTU	P96289 mycobacteri
20	41	61.2	999	2 Q7N1E3	Q7N1E3 glaucobacter
21	40	59.7	171	2 Q8HG38	Q8HG38 alligator b
22	40	59.7	205	2 Q6LOE6	Q6LOE6 pictophilus
23	40	59.7	213	2 Q72S22	Q72S22 xenopus lae
24	40	59.7	232	1 CYSH_SYNP7	Q55309 synchococc
25	40	59.7	288	2 Q8KMM1	Q8KMM1 leucocostoc
26	40	59.7	288	2 CAD24411	CAD24411 leucocostoc
27	40	59.7	284	2 Q31016	Q31016 vibrio angu
28	40	59.7	322	1 FA8H_TROWT	Q83H15 tripheryma
29	40	59.7	462	2 Q8BRE3	Q8BRE3 mus musculu
30	40	59.7	492	2 Q9A7D4	Q9A7D4 cauliobacter
31	40	59.7	555	2 Q754E9	Q754E9 ashbya goss

32	40	59.7	555	2 AAS53492	AAS53492 ashbya go
33	40	59.7	579	2 Q9KPJ7	Q9KPJ7 vibrio chol
34	40	59.7	623	2 Q7TMM1	Q7TMM1 mus musculu
35	40	59.7	681	2 Q8C751	Q8C751 mus musculu
36	40	59.7	681	2 Q8CFS2	Q8CFS2 mus musculu
37	40	59.7	745	2 Q86VR6	Q86VR6 homo sapien
38	40	59.7	826	2 Q9VX34	Q9VX34 drosophila
39	40	59.7	875	1 DD10_HUMAN	Q13306 homo sapien
40	40	59.7	891	2 Q80Y44	Q80Y44 mus musculu
41	40	59.7	1617	2 Q9SKV5	Q9SKV5 arabidopsis
42	39	58.2	111	2 Q92MB6	Q92MB6 rhizobium m
43	39	58.2	129	2 Q7R2L8	Q7R2L8 giardia lam
44	39	58.2	200	2 Q89DD4	Q89DD4 bradyrhizob
45	39	58.2	220	2 Q9ZKAS	Q9ZKAS helicobacte

ALIGNMENTS

RESULT 1					
ID	Q8U787	PRELIMINARY;	PRT;	382 AA.	
AC	Q8U787;				
DT	01-JUN-2002 (Tremblrel. 21, Created)				
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Transcriptional regulator, ROK family.				
GN	OrderedlocusNames=Atu4567;				
OC	Agrobacterium tumefaciens (strain C58 / ATCC 33970).				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.				
OX	NCBI_Taxid=176299;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Dupont;				
RX	MEDLINE=21608550; PubMed=11743193;				
RA	Wood D.W., Secubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,				
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,				
RA	Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,				
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,				
RA	Kutyavlin T., Levy R., Li M.-J., McClelland E., Palmeri P., Gordon D.,				
RA	Raymond C., Rouse G., Saenphimmachak C., Wu Z., Krespan W., Perry M.,				
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,				
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,				
RA	Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,				
RT	Nester E.W.;				
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens				
RT	C58."				
RL	Science 294:2317-2323 (2001).				
DR	EMBL; AE009385; AAL45361.1; -.				
DR	PIR; AC3116; AC3118.				
DR	PIR; D98169; D98169.				
DR	InterPro; IPR000600; ROK.				
DR	InterPro; IPR009058; Wing_hlx_DNA_bnd.				
DR	Pfam; PF00480; ROK. 1.				
KW	Complete proteome.				
SO	SEQUENCE 382 AA; 42285 MW; 77DF5D6C2F279C20 CRC64;				
Query Match					
		68.7%;	Score 46;	DB 2;	Length 382;
		Best Local Similarity .80.0%;	Pred. No. 22;		
	Matches 8;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	2 FEGAGLVGQ 11				
DB	226 FEGAGLVGQ 235				
RESULT 2					
ID	Q7CVA1	PRELIMINARY;	PRT;	402 AA.	
AC	Q7CVA1;				
DT	05-JUL-2004 (Tremblrel. 27, Created)				
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)				

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE AGR L.609p.
GN OrderedLocNames=AGR_L_609;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Houtell B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houliet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Woliam C., Allinger M., Doughy D., Scott C., Lappe C., Markelz B.,
RA Flanagan C., Crowell C., Guron J., Lomo C., Sear C., Strub G.,
RA Cleo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AB008230; AKK8878.1; -.
DR InterPro: IPR000600; ROK.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00480; ROK; 1.
SQ SEQUENCE 402 AA; 44410 MW; EF4426C3B616A820 CRC64;

Query Match 68.7%; Score 46; DB 2; Length 402;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEGAGVLGGQ 11
Db 246 FEGAGVLGGQ 255

RESULT 3
NIFI_KLEBN STANDARD; PRT; 1171 AA.
ID NIFI_KLEBN
AC P03833; P09112;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-).
GN Name=nifj;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89094839; PubMed=3062178;
RA Arnold W., Rump A., Klipp W., Pfeifer U.B., Puehler A.;
RT "Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the
RT entire nitrogen fixation gene cluster of Klebsiella pneumoniae."
RL J. Mol. Biol. 203:715-738(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083580; PubMed=3060860;
RA Cannon M., Cannon F., Buchanan-Mollaston V., Alley D., Alley A.,
RA Beynon J.;
RT "The nucleotide sequence of the nifD gene of Klebsiella pneumoniae."
RL Nucleic Acids Res. 16:11379-11379(1988).
RN [3]
RP REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE=93247479; PubMed=8483412;
RA Charlton W., Cannon W., Buck M.;
RA "The Klebsiella pneumoniae nifD promoter: analysis of promoter
RT elements regulating activation by the NifA promoter."
RL Mol. Microbiol. 7:1007-1021(1993).
RN [4]
RP SEQUENCE OF 1-127 FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S., Xue Z., Kong Q., Wu Q.;

```

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RT "An open reading frame upstream from the nifH gene of Klebsiella
RT pneumoniae."
RL Nucleic Acids Res. 11:4241-4250(1983).
CC -1- FUNCTION: Oxidoreductase required for the transfer of electrons
CC from pyruvate to flavodoxin, which reduces nitrogenase.
CC -1- CATALYTIC ACTIVITY: Pyruvate + COA + oxidized flavodoxin = acetyl-
CC CoA + CO(2) + reduced flavodoxin.
CC -1- SIMILARITY: The iron-sulfur centers are similar to those of
CC bacterial-type 4Fe-4S ferredoxins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: X01007; CA25502.1; -.
DR EMBL: X13303; CA31665.1; -.
DR EMBL: X13109; CA31501.1; -.
DR PIR: S01997; OOKBPP.
DR HSSP: P94692; 1XKK.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR009051; Helical_ferredoxn.
DR InterPro: IPR002869; POR.
DR InterPro: IPR00399; Pyruvate decarb.
DR InterPro: IPR009014; Transketol_C-like.
DR Pfam: PF00037; Fer4_2.
DR Pfam: PF01855; POR_N; 1.
DR Pfam: PF02775; TPP_enzyme_C; 1.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Electron transport; Iron-sulfur; Nitrogen fixation;
KW Oxidoreductase.
FT METAL 691 691 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 694 694 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 697 697 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 701 701 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 745 745 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 748 748 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 751 751 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 755 755 Iron-sulfur 1 (4Fe-4S) (Potential).
FT CONFLICT 406 406 A -> R (in Ref. 2).
SQ SEQUENCE 1171 AA; 128041 MW; 95796232AD11012C CRC64;

Query Match 68.7%; Score 46; DB 1; Length 1171;
Best Local Similarity 72.7%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEGAGVLGGQ 11
Db 873 FEGAGVLGGQ 883

RESULT 4
ID Q755M3 PRELIMINARY; PRT; 160 AA.
AC Q755M3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE AFL209WP.
GN Name=AFL209W;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;

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RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flaviter A.,
 RA Gaffney T.D., Philippen P.,
 RT "The Asbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016899; AAS53165.1; -.
 DR AGD; AFL209W; -.
 SQ SEQUENCE 160 AA; 17720 MW; 38527868AB7B092E CRC64;

Query Match 62.7%; Score 42; DB 2; Length 160;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAGLVGGGF 12
 DB 149 GAGTTLGGGF 158

RESULT 5
 AAS53165 PRELIMINARY; PRT; 160 AA.
 AC AAS53165;
 DT 23-APR-2004 (TrEMBLrel. 27, Created)
 DT 23-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 23-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AFL209WP.
 GN AFL209W.
 OS Asbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flaviter A.,
 RA Gaffney T.D., Philippen P.,
 RT "The Asbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016899; AAS53165.1; -.
 SQ SEQUENCE 160 AA; 17720 MW; 38527868AB7B092E CRC64;

Query Match 62.7%; Score 42; DB 2; Length 160;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAGLVGGGF 12
 DB 149 GAGTTLGGGF 158

RESULT 6
 Q9RS23 PRELIMINARY; PRT; 396 AA.
 AC Q9RS23;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DR2304.
 GN OrderedLocNames=DR2304;
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathavan J.J., Lam P., McDonald L.A., Uterback T.R., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
 RA Frazer C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002062; AAF11854.1; -.
 DR PIR; B75290; B75290.
 DR TIGR; DR2304; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 396 AA; 39229 MW; 355FCB5E0179F312 CRC64;

Query Match 62.7%; Score 42; DB 2; Length 396;
 Best Local Similarity 88.9%; Pred. No. 11e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
 DB 264 FGAGFVLGG 272

RESULT 7
 Q6CC56 PRELIMINARY; PRT; 540 AA.
 AC Q6CC56;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Chromosome C of strain CL1899 of Yarrowia lipolytica.
 GN ORFNames=VALI0C12342g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1899;
 RG GENOLEVRES;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Catolico L., Confanieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Leduc I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolski M., Oza S., Olier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1899;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382129; CAG82066.1; -.
 SQ SEQUENCE 540 AA; 58440 MW; BCCAB9595C981AF CRC64;

Query Match 62.7%; Score 42; DB 2; Length 540;
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
 DB 342 EFGAKTVLGGK 352

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RESULT 8
O92P15 PRELIMINARY; PRT; 155 AA.
ID O92P15
AC O92P15;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE HYDROTHERMAL TRANSMEMBRANE SIGNAL PEPTIDE PROTEIN.
GN OrderedlocusNames=R01982; ORFNames=SMC04336;
OS Rhizobium meliloti (Sinorhizobium meliloti);
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Batloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kallman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masny D., Palm C., Peck M.C., Pohl T.W., Portetelle D., Purnelle B.,
RA Ramsberger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL Science 293:668-672(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=2136507; PubMed=11481430;
RA Capela D., Batloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsberger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46561.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
KM Complete proteome; Hypothetical protein; Transmembrane.
SQ SEQUENCE 155 AA; 17944 MW; 0A3E12286D1FDAFA CRC64;

Query Match 61.2%; Score 41; DB 2; Length 155;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FGAGVIVGG 10
Db 93 FGAGMITIG 101

RESULT 9
O84633 PRELIMINARY; PRT; 291 AA.
ID O84633;
AC O84633;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase.
GN Name=19PA; OrderedlocusNames=CT628;
OS Chlamydia trachomatis;
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / UM-3 / Cx;
RX MEDLINE=99000809; PubMed=9794136;
RA Stephens R.S., Kallman S., Lammel C.J., Fan J., Marache R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

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RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AE001333; AAC68232.1; -.
DR PIR; E71491; E71491.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR InterPro; IPR000092; Polyprenyl_synth.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF00348; polyprenyl_synth; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
DR PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
KM Complete proteome.
SQ SEQUENCE 291 AA; 32550 MW; C257BF3929D5F839 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 291;
Best Local Similarity 63.6%; Pred. No. 1,2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FGAGVIVGGOF 12
Db 153 FGAGVILGGOF 163

RESULT 10
ATX2 YEAST
ID ATX2 YEAST STANDARD; PRT; 313 AA.
AC 012067;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Metal homeostasis factor ATX2.
GN Name=ATX2; OrderedlocusNames=YOR079C; ORFNames=YOR29-30;
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97042460; PubMed=8887660;
RA Lin S.-J., Culotta V.C.;
RT "Suppression of oxidative damage by Saccharomyces cerevisiae ATX2,
RT which encodes a manganese-traffic protein that localizes to Golgi-
RT like vesicles.";
RL Mol. Cell. Biol. 16:6303-6312(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97279235; PubMed=9133743;
RA Valens M., Bonn C., Dalgman-Fornier B., Dang V., Bolotin-Fukuhara M.;
RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the
RT presence of two tRNAs and 24 new open reading frames.";
RL Yeast 13:379-390(1997).
CC -!- FUNCTION: Functions in the homeostasis of manganese ions.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. GO:gl.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; U46033; AAB37236.1; -.
DR EMBL; Z74987; CAA9272.1; -.
DR EMBL; Z70678; CAA94564.1; -.
DR PIR; S66962; S66962.
DR GenOnline; 143667; -.
DR SGD; S0005605; ATX2.
DR GO; GO:0000139; C:Golgi membrane; IDA.
DR GO; GO:0005384; F:manganese ion transporter activity; IGI.
DR GO; GO:0030026; P:manganese ion homeostasis; IGI.
DR InterPro; IPR003689; Zn_transpt_Zip.

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DR Pfam; PF02535; Zip; 1.
 KW Golgi stack; Transmembrane.
 FT TRANSMEM 3 23 Potential.
 RT TRANSMEM 68 88 Potential.
 FT TRANSMEM 104 124 Potential.
 FT TRANSMEM 155 175 Potential.
 FT TRANSMEM 184 204 Potential.
 FT TRANSMEM 218 238 Potential.
 FT TRANSMEM 252 272 Potential.
 FT TRANSMEM 286 306 Potential.
 SQ SEQUENCE 313 AA; 34408 MW; 81DAEF0B4692268 CRC64;

Query Match 61.2%; Score 41; DB 1; Length 313;
 Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 DB 73 QFGIGMLGTSPM 85

RESULT 11
 AAS56363 PRELIMINARY; PRT; 313 AA.
 ID AAS56363;
 AC AAS56363;
 DT 25-MAR-2004 (TREMBLrel. 27, Created)
 DT 25-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 25-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE YOR079C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marxschky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
 RA Hu Y., Vanberg F., Weger J., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzalez L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Laber J.,
 RA "Creation of the YFLX clone resource: cloning of Saccharomycetes
 RT cerevisiae ORFs in the Gateway recombinational cloning system.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY55037; AAS56363.1; -
 SQ SEQUENCE 313 AA; 34408 MW; 81DAEF0B4692268 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 313;
 Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 DB 73 QFGIGMLGTSPM 85

RESULT 12
 Q82N27 PRELIMINARY; PRT; 319 AA.
 ID Q82N27;
 AC Q82N27;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative sugar kinase.
 GN OrderedLocNames=SAV1476;
 OS Streptomyces avermitilis.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 CX NCBI_TaxId=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948;
 Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.,
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP05027; BAC69186.1; -
 DR GO:0016301; P:kinase activity; IEA.
 DR InterPro: IPR006000; ROK.
 DR Pfam: PF00480; ROK; 1.
 DR PROSITE: PS01125; ROK; 1.
 KW Complete proteome; Kinase.
 SQ SEQUENCE 319 AA; 31301 MW; A0BEF6DA6A38FD29 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 319;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GAGVLVGGQ 11
 DB 143 GGGVLVGGQ 151

RESULT 13
 Q6FWS6 PRELIMINARY; PRT; 331 AA.
 ID Q6FWS6;
 AC Q6FWS6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Similar to gp[Q12067 Saccharomyces cerevisiae YOR079C Metal
 DE homeostasis factor.
 GN ORFNames=CAGL0K0577g;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CX NCBI_TaxId=5478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG GENOLEVURES;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lalonde I., de Montigny J., Marck C., Nevegilise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babbour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissiere A., Boyer J., Cattolico L., Confalonieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogiropoulos O.,
 RA Pellenn S., Potier S., Richard G.F., Strub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Jouvel M., Westhof E., Wirth B.,
 RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
 RA Wincker P., Souciet J.L.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL: CR380957; CAG61429.1; -
 DR InterPro: IPR003689; Zn_transp_zip.
 DR Pfam: PF02535; Zip; 1.
 SQ SEQUENCE 331 AA; 36113 MW; F8337EFPDF1B0E0 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 331;
 Best Local Similarity 53.8%; Pred. No. 1.4e+02;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 49 QFGVGMILGTAFM 61

RESULT 14

Q916G8 PRELIMINARY; PRT; 347 AA.

AC Q916G8; 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Probable binding protein component of ABC transporter.
 GN OrderedocunNames=PA0323;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; Pubmed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL: AE004470; AAG03712.1; -.
 DR PIR: D83605; D83605.
 DR HSSP: P31133; 1A99.
 DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001188; SPTm/putr-bndng.
 DR Pfam: PF01547; SBP_bac.1; 1.
 DR PRINTS: PR00909; SPERMNDNBDNG.
 KW Complete proteome.
 SQ SEQUENCE 347 AA; 38901 MW; 74B371F8684D183C CRC64;

Query Match 61.2%; Score 41; DB 2; Length 347;

Best Local Similarity 80.0%; Pred. No. 1.5e+02; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FGAAGLVIGGQ 11
 Db 11 FGAAGLVIGGQ 20

RESULT 15

Q74EW6 PRELIMINARY; PRT; 444 AA.

AC Q74EW6; 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE NADH oxidase, putative.
 GN ORFNames=GSU0843;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX Pubmed=14671304; DOI=10.1126/science.1088727;
 RA Methé B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,

RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uitterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments."
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017180; AAR34173.1; -.
 DR TIGR: GSU0843; -.
 DR InterPro: IPR001327; PAD_pyr_redox.
 DR InterPro: IPR001037; Pyridine_redox_2.
 DR InterPro: IPR001100; Pyr_redox.
 DR InterPro: IPR004099; Pyr_redox_dim.
 DR Pfam: PF00070; Pyr_redox_1.
 DR Pfam: PF02852; Pyr_redox_dim_1.
 DR PRINTS: PR00368; FADPVR.
 DR PRINTS: PR00411; PNDRDTASEI.
 DR PRINTS: PR00469; PNDRDTASEII.
 SQ SEQUENCE 444 AA; 47967 MW; 8F86F154DC054C94 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 444;

Best Local Similarity 61.5%; Pred. No. 1.8e+02; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 378 EKGTGLLGQWV 390

RESULT 16

AAR34173 PRELIMINARY; PRT; 444 AA.

AC AAR34173; 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE NADH oxidase, putative.
 GN GSU0843.
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX Pubmed=14671304;
 RA Methé B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J., Khouri H.M., Feldblyum T.V., Uitterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments."
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017209; AAR34173.1; -.
 DR TIGR: GSU0843; -.
 SQ SEQUENCE 444 AA; 47967 MW; 8F86F154DC054C94 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 444;

Best Local Similarity 61.5%; Pred. No. 1.8e+02; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 378 EKGTGLLGQWV 390

RESULT 17

YF89_YEAST

```

ID YFE9 YEAST STANDARD; PRT; 623 AA.
AC P43554;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 70.3 kDa protein in ABR2-EMP47 intergenic region.
GN OrderedLOCusNames=YFL049W;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M.-A., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RT Nucleic Acids Res. 23:261-268(1995).
RL Net. Genet. 10:261-268(1995).
CC -1- SIMILARITY: TO YEAST NP16.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; D50617; BAA09192.1; -.
DR PIR; S56206; S56206.
DR GEMSTONE; 140107; -.
DR SGD; S0001845; YFL049W.
DR GO; GO:0005634; C:nucleus; IDA.
DR Hypothetical protein.
KW SEQUENCE 623 AA; 70275 MW; A8AC00CAC8F0ED0E CRC64;
SQ
Query Match 61.2%; Score 41; DB 1; Length 623;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 194 EFGAGLVLAGSQ 204
RESULT 18
06FPT7 PRELIMINARY; PRT; 765 AA.
AC 06FPT7;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Similar to sp|P20448 Saccharomyces cerevisiae YJ01033W HCA4.
GN ORFNames=CAGL01045G;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG GUNOLEVRES;
RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Fringuel L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrans A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozzul R., Lemaire M., Leduc I., Ma L., Muller H.,

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RA Nicaud J.M., Nikolski M., Oza S., Olier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Strub M.L., Suleau A.,
RA Swennens D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissendach J.,
RA Wincker P., Souclet J.L.;
RT "Genome evolution in yeasts."
RT Nature 430:35-44(2004).
RL EMBL; CR380956; CAG60704.1; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD_box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN 1.
DR ATP-binding; Helicase; Hydrolase.
KW SEQUENCE 765 AA; 87380 MW; A0FDB5879E63504B CRC64;
SQ
Query Match 61.2%; Score 41; DB 2; Length 765;
Best Local Similarity 63.6%; Pred. No. 2.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 141 QFSAGLVLAGK 151
RESULT 19
MML7 MYCTU STANDARD; PRT; 920 AA.
ID MML7 MYCTU
AC P96259;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Putative membrane protein mmpL7.
GN Name=mmpL7; OrderedLOCusNames=RV2942, MT3012, MD2967;
GN ORFNames=MTCY24G1.07C;
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulterson J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RT Nature 393:537-544(1998).
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Ullrich T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).

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RN [3]
RP SPECIES=M.bovis; STRAIN=AP2122/97;
RC MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Sighele R., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duhoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parthill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
RA "The complete genome sequence of Mycobacterium bovis."
RT Proc. Natl. Acad. Sci. U S A. 100:7877-7882(2003).
RL -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the mmpL family.
CC -----
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CC -----
DR EMBL; BX842581; CAB06107.1; -
DR EMBL; AE007123; AA47339.1; -
DR EMBL; BX248344; CAD96654.1; -
DR PIR; C70668; C70668.
DR TIGR; MT3012; -
DR Tuberculist; Rv2942; -
DR InterPro; IPR004869; MMP_L.
DR Pfam; PF03176; MMP_L; 1.
KM Complete proteome; Hypothetical protein; Transmembrane.
FT FT 44 64
FT TRANSMEM 210 230 Potential.
FT TRANSMEM 241 261 Potential.
FT TRANSMEM 271 291 Potential.
FT TRANSMEM 311 331 Potential.
FT TRANSMEM 344 364 Potential.
FT TRANSMEM 389 409 Potential.
FT TRANSMEM 761 781 Potential.
FT TRANSMEM 790 810 Potential.
FT TRANSMEM 822 842 Potential.
FT TRANSMEM 864 884 Potential.
FT TRANSMEM 888 908 Potential.
SQ SEQUENCE 920 AA; 95121 MW; 019FCA9294A854D2 CRC64;

Query Match
Best Local Similarity 61.2%; Score 41; DB 1; Length 920;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 2 FGAGLVN--GGQF 12
Db 876 FGAGLVNVSQGSF 888

RESULT 20
Q7NJE3 PRELIMINARY; PRT; 999 AA.
AC 07NJE3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE G11889 protein.
GN OrderedLocustNames=G11889;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;
RA MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Miura M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;

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RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids."
RL DNA Res. 10:137-145(2003).
DR EMBL; AP006574; BAC89830.1; -
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0003777; F:mitochondrial motor activity; IEA.
DR InterPro; IPR002151; Kinesin_light.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 9.
DR PRINTS; PRO0381; KINESINLIGHT.
DR PROSITE; PS50005; TPR; 6.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 999 AA; 109847 MW; EDEFA1239AB564B5 CRC64;

Query Match
Best Local Similarity 72.7%; Score 41; DB 2; Length 999;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EFGAGLVG3Q 11
Db 901 EFGAGLVG3E 911

RESULT 21
Q8HG38 PRELIMINARY; PRT; 171 AA.
AC 08HG38;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
OS Alligator sinensis (Chinese alligator).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Alligatorine; Alligator.
OX NCBI_TaxID=38654;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Wang Y., Zhou K., Zhu W., Nie J., Wang C., Xie W.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF511507; AAN84928.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006130; P:mitochondrial electron transport, NADH to u. .; IEA.
DR InterPro; IPR004157; Oxidored_g3.
DR Pfam; PF00499; Oxidored_g3; 1.
KM Mitochondrion.
SQ SEQUENCE 171 AA; 18603 MW; 51012386670FAF3 CRC64;

Query Match
Best Local Similarity 59.7%; Score 40; DB 2; Length 171;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 2 FGAGLVN--GGQFM 13
Db 37 FGAGLVNVSQGSFM 50

RESULT 22
Q6LOB6 PRELIMINARY; PRT; 205 AA.
AC 06LOB6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Translation initiation factor 2 beta subunit.
GN OrderedLocustNames=PT00971;
OS Pterophilus torridus.
OC Archaee; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 9790 / ATCC 700027;
 RX PubMed-15184674;
 RA Fueterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
 RA Scheraga B., Dock C., Antimikhan G., Liebl W.,
 RT "Genome sequence of *Picrophilus torridus* and its implications for life
 RT around pH 0."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
 DR EMBL, AB017261; AAT43556.1; -
 DR GO:0003743; F:translation initiation factor activity; IEA.
 DR InterPro: IPR002735; eIF5_eIF2B.
 DR InterPro: IPR002792; TRAM.
 DR Pfam: PF01873; eIF-5_eIF-2B; 1.
 DR Pfam: PF01938; TRAM; 1.
 DR Prodom: PD004078; eIF5_eIF2B; 1.
 DR SMART; SM00653; eIF2B_5; 1.
 DR PROSITE; PS50926; TRAM; 1.
 KW Complete proteome; Initiation factor.
 SQ SEQUENCE 205 AA; 23266 MW; 5BF3E104D64EA5C6 CRC64;
 Query Match 59.7%; Score 40; DB 2; Length 205;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EFGAGLVLSGQ 11
 DB 66 EFGAGLVLSGQ 76
 RESULT 23
 Q7S22 PRELIMINARY; PRT; 213 AA.
 AC Q7S22;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Claudin7L1 (MGC53400 protein).
 GN Name=cln7L1;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_Taxid=8355;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.,
 RT "Gene expression pattern analysis of the tight junction protein,
 RT Claudin, in the early morphogenesis of *Xenopus* embryos."
 RL Gene Expr. Patterns 2:23-26(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik A.K., Farmer A.A., Rubin J.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalton D.E., Schmechel A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for *Xenopus* research. The NIH *Xenopus*
 RT Initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AB072910; BAC21015.1; -
 DR EMBL, BC048771; AH48771.1; -
 DR GO:0016021; C:integral to membrane; IEA.
 DR GO:0005923; C:tight junction; IEA.
 DR GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR006187; Claudin.
 DR InterPro: IPR003552; Claudin7.
 DR InterPro: IPR006188; Claudin7eg.
 DR InterPro: IPR004031; PMP22_Claudin.
 DR Pfam: PF00822; PMP22_Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01381; CLAUDIN7.
 DR PROSITE; PS01346; CLAUDIN; 1.
 KW Transmembrane.
 SQ SEQUENCE 213 AA; 22731 MW; CDDF3E2D804B5775 CRC64;
 Query Match 59.7%; Score 40; DB 2; Length 213;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 QY 1 EFGAGVLIG-
 DB 160 EFGAGVLIGMAGSFL 174
 RESULT 24
 CYSH_SYNP7 STANDARD; PRT; 232 AA.
 AC CYSH_SYNP7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (PAPS
 DE reductase, thioredoxin dependent) (PAPS reductase) (3'-
 DE phosphoadenylylsulfate reductase) (PAPS sulfotransferase).
 GN Name=cysh; Synonyms=par, sea0019;
 OS *Synechococcus* sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
 NCBI_Taxid=1140;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=9309269; PubMed=1463852;
 RX Niehaus A., Gieselmann G., Schenn J.D.,
 RT "Primary structure of the *Synechococcus* PCC 7942 PAPS reductase
 RT gene."
 RL Plant Mol. Biol. 20:1179-1183(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Holtman C.K., Socias T., Mohler B.J., Chen Y., Min H., Golden S.S.,
 RA Yoderlin P.,
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Reduction of activated sulfate into sulfite.
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-bisphosphate + sulfite +
 CC oxidized thioredoxin = 3'-phosphoadenylyl sulfate + reduced
 CC thioredoxin.
 CC -1- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
 CC branch; third step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the PAPS reductase family. Cysh subfamily.

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CC -----
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CC -----
DR EMBL; M84476; AAA27328.1; -.
DR EMBL; U30252; AAL03931.1; -.
DR PIR; S28609; S28609.
DR HSSP; P17854; ISUR.
DR HAMAP; MF_00063; -. 1.
DR InterPro; IPR004511; CysH.
DR InterPro; IPR002500; PAPS_reduct.
DR Pfam; PF01507; PAPS_reduct; 1.
DR TIGRPFAMs; TIGR00434; CysH; 1.
KW Cysteine biosynthesis; Oxidoreductase.
FT CONFLICT 218 218 T -> S (in Ref. 2).
SQ SEQUENCE 232 AA; 26636 MW; 549FECB3BF8FD CRC64;

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Query Match          59.7%; Score 40; DB 1; Length 232;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 EFGAGLVGGQF 12
Db 30 EFGAGLVGGQF 41

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RESULT 25
Q8KMM1 ID 08KMM1 PRELIMINARY; PRT; 288 AA.
AC 08KMM1;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Putative fructokinase (EC 2.7.1.4).
GN Name=fruk;
OS Leuconostoc pseudomesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=33968;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC-12291;
RL Helanto M.E.K., Airaksinen U., von Weymarn N., Leisola M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ431694; CAD24411.4; -.
DR GO; GO:000865; F:fructokinase activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR006000; ROK.
DR Pfam; PF00480; ROK; 1.
DR PROSITE; PS01125; ROK; UNKNOWN_1.
KW Kinase; Transferase.
SQ SEQUENCE 288 AA; 31442 MW; F44974CFE8E953B1 CRC64;

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Query Match          59.7%; Score 40; DB 2; Length 288;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 GAGLVGGQFM 13
Db 136 GAGLVGGQFM 146

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RESULT 26
CAD24411 ID CAD24411 PRELIMINARY; PRT; 288 AA.
AC CAD24411;
DT 12-MAY-2004 (TREMblrel. 27, Created)
DT 12-MAY-2004 (TREMblrel. 27, Last sequence update)

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DT 12-MAY-2004 (TREMblrel. 27, Last annotation update)
DE Putative fructokinase (EC 2.7.1.4).
GN FRUK.
OS Leuconostoc pseudomesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=33968;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC-12291;
RL Helanto M.E.K., Airaksinen U., von Weymarn N., Leisola M.;
RL "characterization of random mutant strain of Leuconostoc
RT pseudomesenteroides that cannot grow on fructose and its use in
RT mannitol production.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ431694; CAD24411.4; -.
KW Kinase; Transferase.
SQ SEQUENCE 288 AA; 31442 MW; F44974CFE8E953B1 CRC64;

```

```

Query Match          59.7%; Score 40; DB 2; Length 288;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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```

QY 3 GAGLVGGQFM 13
Db 136 GAGLVGGQFM 146

```

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RESULT 27
O31016 ID O31016 PRELIMINARY; PRT; 294 AA.
AC O31016;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Putative rhamnosyl transferase.
GN Name=orf33x8;
OS Vibrio anguillarum (Listonella anguillarum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Listonella.
OX NCBI_TaxID=55601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85-3954-2;
RL Jedani K.E., Stroeder U.H., Manning P.A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF025396; AAB81635.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_trans_2.
DR InterPro; IPR006446; Rhamnosyltran.
DR Pfam; PF00535; Glycos_transf_2; 1.
DR TIGRPFAMs; TIGR01556; Rhamnosyltran; 1.
KW Transferase.
SQ SEQUENCE 294 AA; 33782 MW; 7ABC8A43467CB02C CRC64;

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Query Match          59.7%; Score 40; DB 2; Length 294;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EFGAGLVGGQF 12
Db 111 EFGAGLVGGQF 122

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RESULT 28
FABH_TROWT ID FABH_TROWT STANDARD; PRT; 322 AA.
AC Q83HL5; Q83N01;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein) synthase III (EC 2.3.1.41) (Beta-
DE ketoacyl-ACP synthase III) (KAS III).
GN Name=fabh; OrderedLocustNames=TW1253, TW517;

```


RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 CC EMBL; AK045032; BAC32191.1; -.
 DR MGD; MGI:1924841; Ddx10.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD_box.
 DR InterPro; IPR01650; Helicase_C.
 DR Pfam; PF00270; DEAD_1.
 DR Pfam; PF00271; Helicase_C_1.
 DR SMART; SM00487; DEXDC_1.
 DR SMART; SM00490; HELICG_1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KW ATP-binding; Helicase; Hydrolase.
 FT NON TER 462 462
 SQ SEQUENCE 462 AA; 53099 MW; A3F94D2A15FE645 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 462;
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGQG 11
 DB 169 DFGAGLVIGK 179

RESULT 30
 ID 09A7D4 PRELIMINARY; PRT; 492 AA.
 AC 09A7D4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein CCI1789.
 GN OrderedLocustNames=CCI1789;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nieman W.C., Feilblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
 RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
 RA Frazer C.M.;
 RA "Complete genome sequence of Caulobacter crescentus."
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005853; AAK23765.1; -.
 DR PIR; A87471; A87471.
 DR TIGR; CC1789; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 492 AA; 52155 MW; 1AC33E2A9050D5A CRC64;

Query Match 59.7%; Score 40; DB 2; Length 492;
 Best Local Similarity 77.8%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EFGAGLVGQG 10
 DB 2 EFGAGLVGQG 10

DB 93 FGAUGTIGG 101

RESULT 31
 ID 0754E9 PRELIMINARY; PRT; 555 AA.
 AC 0754E9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AFR121WP.
 GN Name=AFR121W;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dierich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016901; AAS53492.1; -.
 DR AGD; AFR121W; -.
 SQ SEQUENCE 555 AA; 65009 MW; 77A6D92DD6AFB3B8 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 555;
 Best Local Similarity 61.5%; Pred. No. 3.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFGAGLVGQFM 13
 DB 38 EFGAGLVGQFM 50

RESULT 32
 ID AAS53492 PRELIMINARY; PRT; 555 AA.
 AC AAS53492;
 DT 23-APR-2004 (TREMBlrel. 27, Created)
 DT 23-APR-2004 (TREMBlrel. 27, Last sequence update)
 DT 23-APR-2004 (TREMBlrel. 27, Last annotation update)
 DE AFR121WP.
 GN AFR121W.
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dierich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016901; AAS53492.1; -.
 DR EMBL; AE016901; AAS53492.1; -.
 SQ SEQUENCE 555 AA; 65009 MW; 77A6D92DD6AFB3B8 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 555;
 Best Local Similarity 61.5%; Pred. No. 3.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFGAGLVGQFM 13
 DB 38 EFGAGLVGQFM 50


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RESULT 33
09K9J7 PRELIMINARY; PRT; 579 AA.
ID 09K9J7;
AC 09K9J7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Sensory box/GGDEF family protein.
GN OrderedLocusNames=VC2370;
OS Vibrato cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=E1 for N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwim M.L.,
RA Hodelberg R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483 (2000).
DR EMBL; AE004307; AAF95513.1; -.
DR PIR; B82085; B82085.
DR TIGR; VC2370; -.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001610; GGDEF.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR000700; PAS-associ_C.
DR Pfam; PF00980; GGDEF; 1.
DR Pfam; PF00785; PAC; 1.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00086; PAC; 2.
DR SMART; SM00091; PAS; 2.
DR TIGRfam; TIGR00254; GGDEF; 1.
DR TIGRfam; TIGR00229; sensory_box; 1.
DR PROSITE; PS00887; GGDEF; 1.
DR PROSITE; PS50113; PAC; 2.
DR Complete proteome.
SQ SEQUENCE 579 AA; 65762 MW; 6E37C8B467A46CD6 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 579;
Best Local Similarity 88.9%; Pred. No. 3,4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGCG 10
DB 13 FGAGLVGCG 21

RESULT 34
07TMM1 PRELIMINARY; PRT; 623 AA.
ID 07TMM1;
AC 07TMM1;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ddx10 protein (Fragment).
GN Name=Ddx10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.

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RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.P., Caesavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; BC055481; AAH55481.1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD-box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
DR ATP-binding; Helicase; Hydrolase.
KW NON TER 1
FT NON TER 623
SQ SEQUENCE 623 AA; 70849 MW; F5B6893E71179D94 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 623;
Best Local Similarity 54.5%; Pred. No. 3,6e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ERGAGLVGCG 11
DB 111 ERGAGLVGCG 121

RESULT 35
08C751 PRELIMINARY; PRT; 681 AA.
ID 08C751;
AC 08C751;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA. RIKEN full-length enriched
DE library, clone: D430047D13 product: DEAD/H (Asp-Glu-Ala-Asp/His) box
DE polypeptide 10 (RNA helicase), full insert sequence. (Fragment).
GN Name=Ddx10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 [1] SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC MEDLINE=92279253; PubMed=10349636;
 RX Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning";
 RT Meth. Enzymol. 303:19-44(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC MEDLINE=21085660; PubMed=11217851;
 RX RIKEN PANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC The FANTOM Consortium;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC MEDLINE=20499374; PubMed=11042159;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC MEDLINE=20530913; PubMed=11076861;
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Teshiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimura T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RC Aachari U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiwa S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 DR EMBL; AK052540; BAC35031.1; -
 DR MED; W611924841; Ddx10.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD_box.
 DR InterPro; IPR001650; Helicase_C.

DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC_C; 1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
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 FT NON TER 681 681
 SQ SEQUENCE 681 AA; 77839 MW; EF8B6B62BB6F988 CRC64;
 Query Match 59.7%; Score 40; DB 2; Length 681;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 BRGAGLVVAGQ 11
 DB 169 PDSAGLITGK 179
 RESULT 36
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 AC Q8CF82;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ddx10 protein (Fragment).
 GN Name=Ddx10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 RP TISSUE=Eye;
 RC MEDLINE=22388257; PubMed=12477932;
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 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.S., McKernan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Richardson J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Fahey J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Eye;
 RC Strausberg R.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 DR EMBL; BC023303; AAH23303.1; -
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 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD_box.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.

DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KM ATP-binding; Helicase; Hydrolase.
FT NON_TER 681
SQ SEQUENCE 681 AA; 77877 MW; E79A1870E68FC240 CRC64;
Query Match 59.7%; Score 40; DB 2; Length 681;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EFGAGLVLGQ 11
DB 169 DFSAGLIGGK 179
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ID 086VR6 PRELIMINARY; PRT; 745 AA.
AC 086VR6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DDX10 protein (Fragment).
GN Name-DDX10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC NCBI_TaxID=9606;
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RC TISSUE=Lymph;
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RA Streusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinski M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Streusberg R.,
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; BC049217; AAH49217.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.

DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KM ATP-binding; Helicase; Hydrolase.
FT NON_TER 745
SQ SEQUENCE 745 AA; 85831 MW; F689A0379D1C09CB CRC64;
Query Match 59.7%; Score 40; DB 2; Length 745;
Best Local Similarity 54.5%; Pred. No. 4.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EFGAGLVLGQ 11
DB 169 DFSAGLIGGK 179
RESULT 38
ID 09VX34 PRELIMINARY; PRT; 826 AA.
AC 09VX34;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GN ORFNames=CG5800;
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
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RC MEDLINE=20196006; PubMed=10731132;
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup E.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclab J.M.,
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Waasean D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426055; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

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Search completed: December 9, 2004, 09:20:51
 Job time : 9.96223 secs

RESULT 40

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ID 080Y44; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)

DE Ddx10 protein (Fragment).

GN Name=Ddx10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

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RC TISSUE=Eye;

RX MEDLINE=22388257; PubMed=12477932;

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 Krzywinski M.I., Skalski U., Smalins D.E., Schermer A., Schein J.E.,
 Jones S.J., Matra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.L.

CC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

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DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.

DR GO: GO:0016787; F:hydrolyase activity; IEA.

DR GO: GO:0003676; F:nucleic acid binding; IEA.

DR InterPro: IPR001410; DEAD

DR InterPro: IPR01545; DEAD/DEAH_N

DR InterPro: IPR000629; DEAD_box

DR Pfam: PF00270; DEAD; 1.

DR Pfam: PF00271; Helicase_C; 1.

DR SMART: SM00487; DEXDC; 1.

DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.

DR ATP-binding; Helicase; Hydrolyase.

KW NON_TER

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SEQUENCE 891 AA; 102289 MW; FCCABBEFA9FA5892 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 891;

Best Local Similarity 54.5%; Pred. No. 5e+02;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model1

Run on: December 9, 2004, 08:56:57 ; Search time 1.28597 Seconds
(without alignments)
670.415 Million cell updates/sec

Title: US-09-462-416-1

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Searched: 478139 seqs, 66318000 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
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3	42	62.7	360	4	US-09-252-991A-18909	Sequence 18909, A
4	41	61.2	640	4	US-09-252-991A-27542	Sequence 27542, A
5	40	59.7	171	4	US-09-252-991A-32724	Sequence 32724, A
6	40	59.7	321	4	US-09-270-767-46190	Sequence 46190, A
7	38.5	57.5	903	4	US-09-252-991A-24977	Sequence 24977, A
8	38	56.7	494	4	US-09-252-991A-23386	Sequence 23386, A
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16	36	53.7	239	4	US-09-252-991A-20850	Sequence 20850, A
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ALIGNMENTS

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; Patent No. 6372207
; GENERAL INFORMATION:
; APPLICANT: TEPPER, Mark
; APPLICANT: CUNNINGHAM, Mark
; APPLICANT: SHERRIS, David
; APPLICANT: EL TAYAR, Nabil
; APPLICANT: MCKENNA, Sean
; TITLE OF INVENTION: IPNA2/IPN COMPLEX
; FILE REFERENCE: TEPPER1A.SEO
; CURRENT APPLICATION NUMBER: US/09/215,212
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,295
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C terminal human
US-09-215-212-12
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Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EFGAGLVGGQFM 13
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; Patent No. 6372207
; GENERAL INFORMATION:
; APPLICANT: TEPPER, Mark
; APPLICANT: CUNNINGHAM, Mark
; APPLICANT: SHERRIS, David
; APPLICANT: EL TAYAR, Nabil
; APPLICANT: MCKENNA, Sean
; TITLE OF INVENTION: IPNA2/IPN COMPLEX
; FILE REFERENCE: TEPPER1A.SEO
; CURRENT APPLICATION NUMBER: US/09/215,212
; CURRENT FILING DATE: 1998-12-18
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;; PRIOR APPLICATION NUMBER: 60/068,295
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C terminal human
;; OTHER INFORMATION: SIFMAR2 linked by linker to N terminal human IFNbeta
US-09-215-212-13

Query Match 100.0%; Score 67; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFGAGLVGGQFM 13
Db 6 EFGAGLVGGQFM 18

RESULT 3
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;; Sequence 18909, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 18909
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18909

Query Match 62.7%; Score 42; DB 4; Length 360;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGLVGGQF 12
Db 202 GAGLVGGQF 211

RESULT 4
US-09-252-991A-27542
;; Sequence 27542, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 27542
;; LENGTH: 640
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27542

Query Match 61.2%; Score 41; DB 4; Length 640;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FGAGLVGGQ 11
Db 304 FGAGLVGGQ 313

RESULT 5
US-09-252-991A-32724
;; Sequence 32724, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 32724
;; LENGTH: 171
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32724

Query Match 59.7%; Score 40; DB 4; Length 171;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FGAGLVGG 10
Db 101 FGAGLVGG 109

RESULT 6
US-09-270-767-46190
;; Sequence 46190, Application US/09270767
;; Patent No. 6703491
;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1999-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 46190
;; LENGTH: 321
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
;; FEATURE:
;; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46190

Query Match 59.7%; Score 40; DB 4; Length 321;
Best Local Similarity 54.5%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVGGQ 11
Db 189 DFSAGLVGGK 199

RESULT 7
US-09-252-991A-24977


```

: Sequence 24977, Application US/09252921A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,921A
: PRIORITY FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 24977
: LENGTH: 903
: TYPE: PRt
: ORGANISM: Pseudomonas aeruginosa
: US-09-252-921A-24977

```

Query Match	57.5%	Score 38.5;	DB 4;	Length 903;
Best Local Similarity	64.3%	Pred. No. 4e+02;		
Matches	9;	Conservative	1;	Mismatches 1;
				Indels 3;
				Gaps 1;
QY	2	FGAG---LVGGGF	12	
Db	509	FGAGPALALGGGF	522	

RESULT 8
US-09-252-991A-23386
; Sequence 23386, Application US/09252991A
; Patent No. 6551795

```

: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ. ID NOS: 33142
: SEQ ID NO 23386
:
: LENGTH: 494
: TYPE: PRF
: ORGANISM: Pseudomonas aeruginosa
:
: US-09-252-991A-23386

```

Query Match	56.7%	Score 38 ; DB 4 ;	Length 494 ;
Best Local Similarity	77.8%	Pred. No. 2.5e+02 ;	
Matches	7 ;	Conservative	1 ; Indels 0 ; Gaps 0 ;
QY	3 GAGLVLGQQ 11		
db	398 GGGLVLTGE 406		

```

RESULT 9
US-09-270-767-33609
; Sequence 33609, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33609

```

```

; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33609

```

[illegible]

RESULT 10
US-09-543-681A-7178
; Sequence 7178, Application US/09543681A

```

: APPLICANT: GARY BRETON
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709,1002-001
: CURRENT APPLICATION NUMBER: US/09/543,681A
: CURRENT FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: US 60/128,706
: PRIOR FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 8344
: SEQ ID NO 7178
: LENGTH: 150
: TYPE: PRT
: ORGANISM: Proteus mirabilis
: US-09-543-681A-7178

```

Query Match	55.2%	Score 37	DB 4	Length 150
Best Local Similarity	66.7%	Pred. No. 1e+02		
Matches 6	Conservative 2	Mismatches 1	Indels 0	Gaps 0

```
QY      2 FGAGLVLCG 10
          | |||::||
Db      26 FSAGLITGG 34
```

RESULT 11
US-09-489-039A-11069
; Sequence 11069, Application US/09489039A
; Patent No. 6610836

```

? APPLICANT: Gary Breton et. al
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
? TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 2709.2004001
? CURRENT APPLICATION NUMBER: US/09/489,039A
? CURRENT FILING DATE: 2000-01-27
? PRIOR APPLICATION NUMBER: US 60/117,747
? PRIOR FILING DATE: 1999-01-29
? NUMBER OF SEQ ID NOS: 14342
? SEQ ID NO 11069

```

ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-11069

Query Match	55.2%	Score 37;	DB 4;	Length 443;
Best Local Similarity	63.6%	Pred. No. 3.3e+02;		
Matches	7;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0
QY	2	FGAGLVGGQF	12	
Db	136	FGGGGGLGGEW	146	

RESULT 12

```
US-09-252-991A-31196
; Sequence 31196, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31196
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31196
```

```
Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 452;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 EFGAGLVGGGPM 13
DB 288 EFGAGLVGGGPM 300
```

```
RESULT 13
US-09-252-991A-33065
; Sequence 33065, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33065
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33065
```

```
Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 574;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 FGAAGLVGGGPM 12
DB 136 FGAAGLVGGGPM 146
```

```
RESULT 14
US-09-540-236-2968
; Sequence 2968, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
```

```
; SEQ ID NO 2968
; LENGTH: 153
; TYPE: PRT
; ORGANISM: M.cattarrhalis
US-09-540-236-2968
```

```
Query Match
Best Local Similarity 54.5%; Score 36.5; DB 4; Length 153;
Matches 7; Conservative 4; Mismatches 1; Indels 3; Gaps 1;
```

```
QY 2 FGAAGLVGGGPM 13
DB 21 FGAAGLVGGGPM 35
```

```
RESULT 15
US-09-252-991A-29929
; Sequence 29929, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29929
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29929
```

```
Query Match
Best Local Similarity 53.7%; Score 36; DB 4; Length 213;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 GAGLVGGG 10
DB 143 GAGLVGGG 150
```

```
RESULT 16
US-09-252-991A-20850
; Sequence 20850, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20850
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20850
```

```
Query Match
Best Local Similarity 53.7%; Score 36; DB 4; Length 239;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 EFGAGLVGGG 10
```

Db 162 ELGAGVYAGG 171

RESULT 17

US-09-134-000C-4497
; Sequence 4497, Application US/09134000C
; Patent No. 6617155
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4497
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4497

Query Match 53.7%; Score 36; DB 4; Length 242;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGVL 8
Db 45 EFGAGLV 52

RESULT 18

US-09-252-991A-26774
; Sequence 26774, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26774
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26774

Query Match 53.7%; Score 36; DB 4; Length 278;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAAGLVGGGF 12
Db 158 FGAAGLVGGGF 168

RESULT 19

US-09-252-991A-19484
; Sequence 19484, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19484
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19484

Query Match 53.7%; Score 36; DB 4; Length 473;
Best Local Similarity 77.8%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGLVGGGF 12
Db 109 AGLVGGGF 117

RESULT 20

US-08-845-295A-2
; Sequence 2, Application US/08845295A
; Patent No. 5817490
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; CITY: Kingsport
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,295A
; FILING DATE: 25-April-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,879
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-845-295A-2

Query Match 53.7%; Score 36; DB 2; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGG 10
| |||||

Db 146 GGGVLGG 153

RESULT 21

US-09-140-933-2

Sequence 2, Application US/09140933

Patent No. 6022719

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

NUMBER OF SEQUENCES: 2-Keto-L-Gulonic Acid

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/140,933

FILING DATE: 27-August-98

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 584 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-140-933-2

Query Match 53.7%; Score 36; DB 3; Length 584;

Best Local Similarity 87.5%; Pred. No. 6.3e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGVLGG 10

Db 146 GGGVLGG 153

RESULT 22

US-09-146-661-2

Sequence 2, Application US/09146661

Patent No. 6136575

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu-

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146,661

FILING DATE: 03-September-98

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 584 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-146-661-2

Query Match 53.7%; Score 36; DB 3; Length 584;

Best Local Similarity 87.5%; Pred. No. 6.3e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGVLGG 10

Db 146 GGGVLGG 153

RESULT 23

US-09-150-515-2

Sequence 2, Application US/09150515

Patent No. 6271006

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/150,515

FILING DATE: 09-SEP-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-150-515-2

Query Match 53.7%; Score 36; DB 3; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGVG 10
DB 146 GGGVLVVG 153

RESULT 24
US-09-248-796A-19668
Sequence 19668, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19668

LENGTH: 809
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19668

Query Match 53.7%; Score 36; DB 4; Length 809;
Best Local Similarity 70.0%; Pred. No. 8.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAGLVGVGQ 11
DB 193 FSGGLVTVGCK 202

RESULT 25
US-09-134-000C-6657
Sequence 6657, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6657

LENGTH: 70

TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6657

Query Match 52.2%; Score 35; DB 4; Length 70;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGVG 10

DB 31 FGGLVLVVG 39

RESULT 26
US-09-134-000C-5500
Sequence 5500, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5500

LENGTH: 91

TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5500

Query Match 52.2%; Score 35; DB 4; Length 91;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGVG 10
DB 49 FGGLVLVVG 57

RESULT 27
US-09-248-796A-21582
Sequence 21582, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21582
LENGTH: 97
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-21582

Query Match 52.2%; Score 35; DB 4; Length 97;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGVGQF 12
DB 48 KFGTKLINGERF 59

RESULT 28
US-09-621-976-5202
Sequence 5202, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

```

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5202
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23...-1
US-09-621-976-5202

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 107;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FGAGLVGGQFM 13
Db 80 GAGLVGGGLM 90

RESULT 29
US-09-107-858-22
; Sequence 22, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-22

Query Match
Best Local Similarity 52.2%; Score 35; DB 3; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FASGILGTGFM 88

RESULT 30
US-09-107-858-23
; Sequence 23, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-23
```

```

Query Match
Best Local Similarity 52.2%; Score 35; DB 3; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FSSGILGTGFM 88

RESULT 31
US-09-579-174-22
; Sequence 22, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-22

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FASGILGTGFM 88

RESULT 32
US-09-579-174-23
; Sequence 23, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-23

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FSSGILGTGFM 88

RESULT 33
US-09-247-155-163
```

```

; Sequence 163, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguetere, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 163
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -34..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 81,84,87,131,135,143,156
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
; US-09-247-155-163

```

```

Query Match      52.2%; Score 35; DB 3; Length 196;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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```

QY      3 GAGLVGGGPM 13
DB      176 GAGFIIIGGIV 186

```

```

RESULT 34
; US-07-732-242C-7
; Sequence 7, Application US/07732242C
; Patent No. 5298399
; GENERAL INFORMATION:
; APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
; APPLICANT: Hidaka, Makoto; Nakamura, Akira;
; APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
; TITLE OF INVENTION: Gene of Urease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Friesauf, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72mb
; COMPUTER: IBM PC compatible (NEC PC-9801 RX)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,242C
; FILING DATE: 19910718
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPN 2-210178
; FILING DATE: 10-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert

```

```

; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910532/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEFAX: 236268
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-732-242C-7

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```

Query Match      52.2%; Score 35; DB 1; Length 222;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 FGAGLVIG 9
DB      164 FGAGTVLG 171

```

```

RESULT 35
; US-10-140-002-472
; Sequence 472, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 472
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-002-472

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Query Match      52.2%; Score 35; DB 4; Length 229;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY      3 GAGLVGGGPM 13
DB      176 GAGFIIIGGIV 186

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```

RESULT 36
; US-08-513-974B-52
; Sequence 52, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:

```

APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-52

Query Match 52.2%; Score 35; DB 3; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
Qy 2 FGAG-----LVGGQPM 13
Db 196 FGAGKAVILLAVGGQFL 213
RESULT 37
US-08-513-974B-360
Sequence 360, Application US/08513974B
Patent No. 614139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-360

Query Match 52.2%; Score 35; DB 3; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 FGAG-----LVVGQFM 13
DB 196 FGCGKAUVLAVGQFL 213

RESULT 38
US-09-461-436B-52
Sequence 52, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasunaki Ito
Ryo Fujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angel, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273

FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-461-436B-52

Query Match 52.2%; Score 35; DB 4; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 FGAG-----LVVGQFM 13
DB 196 FGCGKAUVLAVGQFL 213

RESULT 39
US-08-758-621-2
Sequence 2, Application US/08758621
Patent No. 5846821
GENERAL INFORMATION:
APPLICANT: Gueriot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean W.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-099CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-758-621-2

Query Match 52.2%; Score 35; DB 2; Length 339;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVIGGQFM 13
 Db 84 FASGIIIGTGFM 95

RESULT 40
 US-09-107-858-2
 ; Sequence 2, Application US/09107858
 ; Patent No. 6162900
 ; GENERAL INFORMATION:
 ; APPLICANT: Guerinet, Mary Lou et al.
 ; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
 ; FILE REFERENCE: DCI-099CPDV
 ; CURRENT APPLICATION NUMBER: US/09/107,858
 ; CURRENT FILING DATE: 1998-06-30
 ; EARLIER APPLICATION NUMBER: 08/758,621
 ; EARLIER FILING DATE: 1996-11-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-107-858-2

Query Match 52.2%; Score 35; DB 3; Length 339;
 Best Local Similarity 50.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FGAGLVIGGQFM 13
 Db 84 FASGIIIGTGFM 95

Search completed: December 9, 2004, 09:22:45
 Job time : 2.28597 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:56:57 ; Search time 53.714 Seconds
(without alignments)
670.415 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861

Sequence: 1 MLAVGCALLAALLAPGAL.....LILRSFKEFLQSSLRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1921	67.1	552	4	US-09-313-942-8	Sequence 8, Appl1
2	1918	67.0	468	3	US-08-795-4738-5	Sequence 5, Appl1
3	1918	67.0	468	4	US-09-439-856-5	Sequence 5, Appl1
4	1918	67.0	468	6	5171840-2	Patent No. 5171840-2
5	1918	67.0	468	6	5480796-2	Patent No. 5480796-2
6	1910	66.8	360	4	US-09-313-942-15	Sequence 15, App
7	1852	64.7	344	6	5171840-7	Patent No. 5171840-7
8	1852	64.7	344	6	5480796-7	Patent No. 5480796-7
9	1788	62.5	1158	4	US-09-313-942-26	Sequence 26, Appl
10	1783	62.3	1168	4	US-09-313-942-24	Sequence 24, App
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16	1153	40.3	210	3	US-09-043-785-1	Sequence 1, Appl1
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19	938.5	32.8	212	1	US-08-792-0198-9	Sequence 9, Appl1
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23	938.5	32.8	212	3	US-08-795-4738-6	Sequence 6, Appl1
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25	938.5	32.8	212	3	US-09-230-371A-27	Sequence 27, Appl
26	938.5	32.8	212	4	US-09-439-856-6	Sequence 6, Appl1
27	938.5	32.8	212	4	US-09-462-941-13	Sequence 13, Appl

28	938.5	32.8	212	6	5510472-2	Patent No. 5510472
29	935	32.7	317	3	US-08-469-318-145	Sequence 145, App
30	935	32.7	317	3	US-08-468-692A-145	Sequence 145, App
31	935	32.7	317	3	US-08-446-892A-145	Sequence 145, App
32	935	32.7	317	4	US-08-762-227A-145	Sequence 145, App
33	935	32.7	317	5	PCR-US93-01185-145	Sequence 145, App
34	934	32.6	184	1	US-08-567-047-2	Sequence 2, Appl
35	934	32.6	184	2	US-08-567-048-2	Sequence 2, Appl
36	934	32.6	184	6	5186931-1	Patent No. 5186931
37	934	32.6	185	1	US-07-632-070B-1	Sequence 1, Appl
38	934	32.6	185	1	US-07-918-181A-2	Sequence 2, Appl
39	934	32.6	185	1	US-08-231-575-2	Sequence 2, Appl
40	934	32.6	185	1	US-08-246-472A-5	Sequence 2, Appl
41	934	32.6	185	2	US-08-766-650-5	Sequence 5, Appl
42	934	32.6	185	5	PCR-US93-06988-2	Sequence 2, Appl
43	934	32.6	185	6	5186931-2	Patent No. 5186931
44	934	32.6	186	1	US-07-632-070B-2	Sequence 2, Appl
45	934	32.6	186	1	US-07-743-382-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-09-313-942-8
; Sequence 8, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-8

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Query March	67.1%;	Score 1921;	DB 4;	Length 592;
Best Local Similarity	77.1%;	Pred. No. 8e-151;		
Matches 377;	Conservative 22;	Mismatches 44;	Indels 46;	Gaps 5

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Query Match	Similarity	67.0%	Score 1918;	DB 3;	Length 468;
Best Local	Similarity	96.5%	Pred. No. 16-150;	Mismatches 4;	Indels 8; Gaps 1.
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Db      241  PHSWSSFYRLRFELRYAERSKFTTTWVKDLOHHCVIDAMSGLRHVQLPAQEEFG 300
Qy      301  GEMSEMSPRAMGTPWTERSPPAENEVSVPQALITTKDDNIIIFRDSANATSLPYEFMP 360
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Db      357  ----QDSSVPLP 365

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1      RESULT 3
2      US-09-439-856-5
3      / Sequence 5, Application US/09439856
4      / Patent No. 641009
5      / GENERAL INFORMATION:
6      / APPLICANT: Galun, Eithan
7      / APPLICANT: Nahot, Orit
8      / APPLICANT: Blum, Herbert E.
9      / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
10     / TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
11     / NUMBER OF SEQUENCES: 10
12     / CORRESPONDENCE ADDRESS:
13     / ADDRESSEE: Davidson and Kappel, LLC
14     / STREET: 1140 Avenue of the Americas
15     / CITY: New York
16     / STATE: New York
17     / COUNTRY: USA
18     / ZIP: 10036
19     / COMPUTER READABLE FORM:
20     / MEDIUM TYPE: 3.5 inch disk
21     / COMPUTER: IBM PC compatible
22     / OPERATING SYSTEM: PC-DOS/MS-DOS
23     / SOFTWARE: MS-DOS EDITOR
24     / CURRENT APPLICATION DATA:
25     / APPLICATION NUMBER: US/09/439,856
26     / FILING DATE:
27     / CLASSIFICATION:
28     / PRIOR APPLICATION DATA:
29     / APPLICATION NUMBER: 08/795,473
30     / FILING DATE: 11-FEB-1997
31     / ATTORNEY/AGENT INFORMATION:
32     / NAME: Davidson, Clifford M.
33     / REGISTRATION NUMBER: 32,728
34     / REFERENCE/DOCKET NUMBER: 963.1007
35     / TELECOMMUNICATION INFORMATION:
36     / TELEPHONE: (212)-997-1037
37     / TELEFAX: (212)-997-1038
38     / INFORMATION FOR SEQ ID NO: 5:
39     / SEQUENCE CHARACTERISTICS:
40     / LENGTH: 468 amino acids
41     / TYPE: amino acid
42     / TOPOLOGY: unknown
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[illegible]

Db 121 CFRKSPLSNVCEWBGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCOYSQESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Qy 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Db 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Qy 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKDVAAP 373
Db 357 ---QDSSSVPLP 365

RESULT 4
5171840-2
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
5171840-2
; LENGTH: 468

Query Match 67.0%; Score 1918; DB 6; Length 468;
Best Local Similarity 96.5%; Pred. No. 1e-150;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60
Qy 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPOLS 120
Db 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPOLS 120
Qy 121 CFRKSPLSNVCEWBGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCOYSQESQKFSQCLAV 180
Db 121 CFRKSPLSNVCEWBGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCOYSQESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Qy 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Db 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Qy 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKDVAAP 373
Db 357 ---QDSSSVPLP 365

RESULT 5
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
5480796-2
; LENGTH: 468

Query Match 67.0%; Score 1918; DB 6; Length 468;
Best Local Similarity 96.5%; Pred. No. 1e-150;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60
Qy 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPOLS 120
Db 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPOLS 120
Qy 121 CFRKSPLSNVCEWBGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCOYSQESQKFSQCLAV 180
Db 121 CFRKSPLSNVCEWBGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCOYSQESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFSKTOTFOGCGILOPDPANITVTVAARPRLSVTWOD 240
Qy 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Db 241 PSHMNSSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFEQ 300
Qy 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKDVAAP 373
Db 357 ---QDSSSVPLP 365

RESULT 6
US-09-313-942-15
; Sequence 15, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 3.1e-150;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPCGVEPBDNATVHM 60

QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
DB 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
QY 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 7
5171840-7
Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298, 694
FILING DATE: 19-JAN-1989
SEQ ID NO: 7:
LENGTH: 344
5171840-7

Query Match 64.7%; Score 1852; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-145;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
DB 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
QY 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 8
5480796-7
Patent No. 5480796
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/907, 650
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298, 694
FILING DATE: 19-JAN-1989
SEQ ID NO: 7:
LENGTH: 344
5480796-7

Query Match 64.7%; Score 1852; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-145;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
DB 121 CPERKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPPAEDEFQPCQYSGESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGIILQPPDPANITVTVANRPMLSVTWOD 240
QY 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSWNSFYRLRPELRYRARSKTFTTMMVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 9
US-09-313-942-26
Sequence 26, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1158
TYPE: PRT
ORGANISM: Homo sapiens
US-09-313-942-26

Query Match 62.5%; Score 1788; DB 4; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.4e-139;
Matches 331; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRAGRPACTVHLVDPPEEPOLS 120


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Db      181 PEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTWD 240
        |||
Qy      241 PHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFGQ 300
        |||
Db      241 PHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFGQ 300
        |||
Qy      301 GEMSEMSPEAMGTPWTESRSP 322
        |||
Db      301 GEMSEMSPEAMGTPWTESRSP 322
        |||

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RESULT 13
US-09-313-942-16
; Sequence 16, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-16

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Query Match      58.8%; Score 1683; DB 4; Length 315;
Best Local Similarity 99.7%; Pred. No. 1.8e-111;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Db      1  MVAAGCALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Qy      61 VLKPAAGSHPSRWAGMGRRLRLRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
        |||
Db      61 VLKPAAGSHPSRWAGMGRRLRLRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
        |||
Qy      121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCLAV 180
        |||
Db      121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCLAV 180
        |||
Qy      181 PEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTWD 240
        |||
Db      181 PEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTWD 240
        |||
Qy      241 PHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFGQ 300
        |||
Db      241 PHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFGQ 300
        |||
Qy      301 GEMSEMSPEAMGT 313
        |||
Db      301 GEMSEMSPEAMGT 313
        |||

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RESULT 14
5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694

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; FILING DATE: 19-JAN-1989
; SEQ ID NO: 5
; LENGTH: 386
5171840-5

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Query Match      48.5%; Score 1389; DB 6; Length 386;
Best Local Similarity 73.6%; Pred. No. 5.9e-107;
Matches 276; Conservative 1; Mismatches 4; Indels 94; Gaps 4;

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Qy      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Db      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Qy      61 VLKPAAGSHPSRWAGMGRRLRLRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
        |||
Db      28 -----VDVPEEPQLS 38
        |||
Qy      121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCL 178
        |||
Db      39 CFRKSPLSNVV--GPRSTPEMSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCL 96
        |||
Qy      179 AVEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTW 238
        |||
Db      97 AVEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTW 156
        |||
Qy      239 ODRHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFP 298
        |||
Db      157 ODRHSNNSFYILRFELRYARERKSTTTMMVVDLQHHCVTHDAMSGLRHVYQLRAOEFP 216
        |||
Qy      299 GQGESEMSPEAMGTPWTESRSPPAENEYSTPMQALTNKDDNITLFRDSANATSLPVEF 358
        |||
Db      217 GQGESEMSPEAMGTPWTESRSPPAENEYSTPMQALTNKDDNITLFRDSANATSLPVEF 274
        |||
Qy      359 MEVPEGEDSKDYAAP 373
        |||
Db      275 -----QDSSSVPLP 283
        |||

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RESULT 15
5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 5
; LENGTH: 386
5480796-5

```

```

Query Match      48.5%; Score 1389; DB 6; Length 386;
Best Local Similarity 73.6%; Pred. No. 5.9e-107;
Matches 276; Conservative 1; Mismatches 4; Indels 94; Gaps 4;

```

```

Qy      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Db      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
        |||
Qy      61 VLKPAAGSHPSRWAGMGRRLRLRSVOLHDSGNYSCYRAGRPACTVHLVDVPEEPQLS 120
        |||
Db      28 -----VDVPEEPQLS 38
        |||
Qy      121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCL 178
        |||
Db      39 CFRKSPLSNVV--GPRSTPEMSLTTKAVILVRKFQNSPAEDFOEPCCOYSQESQKFSQCL 96
        |||
Qy      179 AVEGDSSFYIVSMCVASSVSGSKSKTQTFQCGIILQDPDPANITVTAVARNPRLSVTW 238
        |||

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DB 97 AVEGDSSFYIVSMCVASSVSGSKFKSTQTFQGGCIIQPPDPANITVTAVARNRMLSVTM 156
 QY 239 QDPHSNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQLRAOEER 298
 DB 157 QDPHSNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQLRAOEER 216
 QY 299 GQGEWSEWSPAMGTPTWTSRSPAPENEVSTPMQALTTNKDDNIIIFRDSANATSLPVER 358
 DB 217 GQGEWSEWSPAMGTPTWTSRSPAPENEVSTPMQALTTNKDDNIIIFRDSANATSLP-- 274
 QY 359 MPVPEGDSKDYAAP 373
 DB 275 -----QDSSSVPLP 283

RESULT 16
 US-09-043-785-1
 ; Sequence 1, Application US/09043785
 ; Patent No. 6172042
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEBATH, Judith
 ; APPLICANT: HALIMI, Hubert
 ; APPLICANT: REVEL, Michel
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
 ; FILE REFERENCE: Chebath-1
 ; CURRENT APPLICATION NUMBER: US/09/043,785
 ; EARLIER FILING DATE: 1998-09-02
 ; EARLIER APPLICATION NUMBER: PCT/1196/00119
 ; EARLIER FILING DATE: 1996-09-26
 ; EARLIER APPLICATION NUMBER: 115,453
 ; EARLIER FILING DATE: 1995-09-26
 ; EARLIER APPLICATION NUMBER: 118,097
 ; EARLIER FILING DATE: 1996-05-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-043-785-1

Query Match 40.3%; Score 1153; DB 3; Length 210;
 Best Local Similarity 100.0%; Pred. No. 9, 2e-88;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 113 PPEEPOLSCFRKSPLSNVCEWGPSTPSLTITKAVILVRKFQNSPAEDFQEPQYSQESQ 172
 DB 1 PPEEPOLSCFRKSPLSNVCEWGPSTPSLTITKAVILVRKFQNSPAEDFQEPQYSQESQ 60
 QY 173 KESCOLAVEGDSSEFIVSMCVASSVSGSKFKSTQTFQGGCIIQPPDPANITVTAVARNR 232
 DB 61 KESCOLAVEGDSSEFIVSMCVASSVSGSKFKSTQTFQGGCIIQPPDPANITVTAVARNR 120
 QY 233 WLSVTWQDPHSNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQL 292
 DB 121 WLSVTWQDPHSNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQL 180
 QY 293 RAQEEFGQGEWSEWSPAMGTPTWTSRSP 322
 DB 181 RAQEEFGQGEWSEWSPAMGTPTWTSRSP 210

RESULT 17
 5171840-11
 ; Patent No. 5171840
 ; APPLICANT: KISHIMOTO, TADAMITSU
 ; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 ; STIMULATORY FACTOR-2
 ; NUMBER OF SEQUENCES: 11
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/298,694
 ; FILING DATE: 19-JAN-1989
 ; SEQ ID NO:11:

LENGTH: 201
 5171840-11
 Query Match 33.2%; Score 950; DB 6; Length 201;
 Best Local Similarity 89.1%; Pred. No. 6e-71;
 Matches 179; Conservative 1; Mismatches 21; Indels 0; Gaps 0;
 QY 123 RKSPLSNVCEWGPSTPSLTITKAVILVRKFQNSPAEDFQEPQYSQESQKFCOLAVE 182
 DB 1 RKSPLSNVCEWGPSTPSLTITKAVILVRKFQNSPAEDFQEPQYSQESQKFCOLAVE 60
 QY 183 GDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQPPDPANITVTAVARNRMLSVTMQDPH 242
 DB 61 GDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQPPDPANITVTAVARNRMLSVTMQDPH 120
 QY 243 SNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQLRAOEFGQGE 302
 DB 121 SNNSFYRLRFELRYAERSKTFETMMVKDLQHCYIHAWGSLRHVVQLRAOEFGQGE 180
 QY 303 WSEWSPAMGTPTWTSRSP 323
 DB 181 WSEWSPAMGTPTWTSRSP 201

RESULT 18
 US-08-716-317-7
 ; Sequence 7, Application US/08716317
 ; Patent No. 5919654
 ; GENERAL INFORMATION:
 ; APPLICANT: HAMA, YUKO
 ; APPLICANT: TOHDA, HIDEKI
 ; APPLICANT: TSUKAMOTO, HIROKO
 ; APPLICANT: MIKAI, KIYOKAZU
 ; APPLICANT: KIMAGAI, HIROMICHI
 ; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
 ; ADDRESS: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/716,317
 ; FILING DATE: 02-OCT-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP96/00198
 ; FILING DATE: 01-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 17167/1995
 ; FILING DATE: 03-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 59-924-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-716-317-7

Query Match 32.8%; Score 939; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4,4e-70;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 MPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESSKEALAE 418
DB 1 MPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESSKEALAE 60
QY 419 NNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQARAQVOMST 478
DB 61 NNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQARAQVOMST 120
QY 479 KVLIOPLQKAKNLDATTPDPPTNASLITKLOQONQWLODMTHLILRSFKERLOSSLR 538
DB 121 KVLIOPLQKAKNLDATTPDPPTNASLITKLOQONQWLODMTHLILRSFKERLOSSLR 180
QY 539 ALRQM 543
DB 181 ALRQM 185

RESULT 19
US-08-792-019B-9
Sequence 9, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUTROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9

Query Match 32.8%; Score 938.5; DB 1; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 354 LPVEF-MPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412
DB 1 LPVEF-MPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412

DB 22 LPAAFPAPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141
QY 473 AVGMSTKVLIOPLQKAKNLDATTPDPPTNASLITKLOQONQWLODMTHLILRSFKER 532
DB 142 AVGMSTKVLIOPLQKAKNLDATTPDPPTNASLITKLOQONQWLODMTHLILRSFKER 201
QY 533 LOSSLRALRQM 543
DB 202 LOSSLRALRQM 212

RESULT 20
US-08-988-819-9
Sequence 9, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUTROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-988-819-9

Query Match 32.8%; Score 938.5; DB 3; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 354 LPVEF-MPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412
DB 22 LPAAFPAPVPPGSDSKVAAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141

QY	473	AVOMSTKVLIQFLOKAKNLDITTPDPPTNASLITXLOAONOMLODMTHILIRSKF	532
Db	142	AVOMSTKVLIQFLOKAKNLDITTPDPPTNASLITXLOAONOMLODMTHILIRSKF	201
QY	533	LOSSLRALROM	543
Db	202	LOSSLRALROM	212

```

RESULT 21
US-09-016-534-9
: Sequence 9, Application US/09016534
: Patent No. 6143874
: GENERAL INFORMATION:
: APPLICANT: CHANG, MING-SHI
: APPLICANT: ELLIOTT, GARY S.
: APPLICANT: SANTIAGO, JULIA
: APPLICANT: SENALDI, GIORGIO
: TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: AMGEN INC.
: STREET: ONE AMGEN CENTER
: CITY: THOUSAND OAKS
: STATE: CA
: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/016,534
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/792,019
: FILING DATE: 03-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: COOK, ROBERT R.
: REGISTRATION NUMBER: 31,602
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..182
: FEATURE:
: NAME/KEY: Region
: LOCATION: -30..0
: US-09-016-534-9

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Query Match	32.8%	Score 938.5	DB 3	Length 212
Best Local Similarity	97.9%	Pred. No. 5.9e-70		
Matches 187	Conservative 0	Mismatches 3	Indels 1	Gaps 1
Qy	354	L P V E F - M V P P G E D S K D V A A P H R O P L T S E R I D K O I R Y I L D I G S A L R K E T C N K S M C C S S	412	
Db	22	L P A A F P A V P P G E G S K D V A A P H R Q L T S E R I D K O I R I L I D I G S A L R K E T C N K S M C C S S	81	
Qy	413	K E A L A E N N L N I P K A E K D G C F O S G F N E E T C L V K I I T G L L E F V Y L E Y I Q N R P S E S E Q A R	472	
Db	82	K E A L A E N N L N I P K A E K D G C F O S G F N E E T C L V K I I T G L L E F V Y L E Y I Q N R P S E S E Q A R	141	
Qy	473	A V O M S T K L I O F L O K K A N L D A I T P P D P T T A S L I T K I Q A O N Q W I Q D M T T H I L S P F E F	532	
Db	142	A V O M S T K L I O F L O K K A N L D A I T P P D P T T A S L I T K I Q A O N Q W I Q D M T T H I L S P F E F	201	

RESULT 22
US-08-097-869-7
Sequence 7, Application US/08097869
Patent No. 6204364
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,869
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,178
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24455-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-097-869-7

Query Match	32.8%	Score 938.5	DB 3	Length 212
Best Local Similarity	97.9%	Pred. No. 5,9e-70		
Matches	187	Conservative	0	Mismatches 3, Indels 1, Gaps 1
QY	354	LPVEP-MPVPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSMCESS	412	
Db	22	LPAPFPAVPPEGSDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSMCESS	81	
QY	413	KEALAENNUNLPKMAEKDGCFOSGFNEBTCVKKITGLLEFEVLEYIQNRPESSEBOAR	472	
Db	82	KEALAENNUNLPKMAEKDGCFOSGFNEBTCVKKITGLLEFEVLEYIQNRPESSEBOAR	141	
QY	473	AVQNSTKYLIFLOKKAINDAITTPDPTNASLITKLOAONQIMQDMTHILIRSFKEF	532	
Db	142	AVQNSTKYLIFLOKKAINDAITTPDPTNASLITKLOAONQIMQDMTHILIRSFKEF	201	
QY	533	LOSSLRALROM 543		
Db	202	LOSSLRALROM 212		

Sequence 6, Application US/08795473B
Patent No. 6217858
GENERAL INFORMATION:
APPLICANT: Galun, Elchan
APPLICANT: Nahot, Orli
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963,1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-795-473B-6

Query Match 32.8%; Score 938.5; DB 3; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
|||
DB 22 LPAAPFAPVPBGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
|||

QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 472
|||
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 141
|||

QY 473 AVQNSTKVLIOFLQKAKNLDATITPPTTNASLITLQANQWLODMTTHLILRSFKEF 532
|||
DB 142 AVQNSTKVLIOFLQKAKNLDATITPPTTNASLITLQANQWLODMTTHLILRSFKEF 201
|||

QY 533 LQSSLRALROM 543
|||
DB 202 LQSSLRALROM 212
|||

RESULT 24
US-09-230-637-45
Sequence 45, Application US/09230637
Patent No. 626458
GENERAL INFORMATION:
APPLICANT: Hayward, Gary
APPLICANT: Nicholas, John
APPLICANT: Hardwick, J. Marie
APPLICANT: Reitz, Marvin
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: Associated Herpesvirus
FILE REFERENCE: 1107,78372
CURRENT APPLICATION NUMBER: US/09/230,637

CURRENT FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/022,591
PRIOR FILING DATE: 1996-07-25
PRIOR APPLICATION NUMBER: PCT US 97/12931
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-09-230-637-45

Query Match 32.8%; Score 938.5; DB 3; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
|||
DB 22 LPAAPFAPVPBGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
|||

QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 472
|||
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 141
|||

QY 473 AVQNSTKVLIOFLQKAKNLDATITPPTTNASLITLQANQWLODMTTHLILRSFKEF 532
|||
DB 142 AVQNSTKVLIOFLQKAKNLDATITPPTTNASLITLQANQWLODMTTHLILRSFKEF 201
|||

QY 533 LQSSLRALROM 543
|||
DB 202 LQSSLRALROM 212
|||

RESULT 25
US-09-230-371A-27
Sequence 27, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohensky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: US93 THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 212
TYPE: PRT
ORGANISM: Human
US-09-230-371A-27

Query Match 32.8%; Score 938.5; DB 3; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
|||
DB 22 LPAAPFAPVPBGEDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
|||

QY 413 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 472
|||
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 141
|||

QY 473 AVQNSTKVLIOFLQKAKNLDATITPPTTNASLITLQANQWLODMTTHLILRSFKEF 532
|||

Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 26

US-09-439-856-6
; Sequence 6, Application US/09439856
; Patent No. 6410009
; GENERAL INFORMATION:
; APPLICANT: Galun, Etchan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,473
; FILING DATE: 11-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-09-439-856-6

Query Match 32.8%; Score 938.5; DB 4; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAFAFAPVPBGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472
Db 82 KEALAENNINLPRMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 532
Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 27

US-09-462-941-13
; Sequence 13, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR FILING DATE: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-462-941-13

Query Match 32.8%; Score 938.5; DB 4; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAFAFAPVPBGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472
Db 82 KEALAENNINLPRMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 532
Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 28
5510472-2
; Patent No. 5510472
; APPLICANT: REVEL, MICHEL; TIOLLAIS, PIERRE
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
; INTERFERON-BETA2
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/883,633
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; APPLICATION NUMBER: 449,447
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 860,883
; FILING DATE: 08-MAY-1986
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; SEQ ID NO: 2
; LENGTH: 212
; 5510472-2

Query Match 32.8%; Score 938.5; DB 6; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAFAFAPVPBGSDSDVAAPHROPLTSSSRIDKQIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472

Db 82 KEAALNNLNPKAEKGGCGGSEFNETCLVITLLEFEVYLLQRRFSSSEQAR 141
QY 473 AVQSTVLIQFLOKRAKNDATITPTTNASLITKLOAQONWLODMTHILIRSFKEF 532
Db 142 AVQSTVLIQFLOKRAKNDATITPTTNASLITKLOAQONWLODMTHILIRSFKEF 201
QY 533 LQSSLRALROM 543
Db 202 LQSSLRALROM 212

RESULT 29

US-08-469-318-145
Sequence 145, Application US/08469318
Patent No. 602535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-318-145

Query Match 32.7%; Score 935; DB 3; Length 317;
Best Local Similarity 63.0%; Pred. No. 2,1e-69;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;
QY 240 DPHSNSSFYRLRFLRYRAERSKTFTTMYKLOH-----HCVIDAWSGAR 287
Db 24 DPNNINSEMDMLIERNLRTPNILAFVR-AVKHLENASGIEALIRNLQPLPSATAPSR 82
QY 288 HVOGLRAQEEFGCGEWS-----PEAMGTPTWT-ESSSPRAENEVSTPMQALTT 336
Db 83 HPILIIKA-----GDWQEFREKLTFLVLTLEQAOEOOYIEGRISPGG----- 125
QY 337 NKDDNLIIFRDSANATSLPVEFMVPPGEDSKVAAPHROPLTSSRIDKQIRYILDGIS 396
Db 126 -----SGGGSNM-----APVPGEDSKVAAPHROPLTSSRIDKQIRYILDGIS 170
QY 397 ALRKETCNKSNMCESSKEALAEANNLNPKAEKGGCGGSEFNETCLVITLLEFEVY 456
Db 171 ALRKETCNKSNMCESSKEALAEANNLNPKAEKGGCGGSEFNETCLVITLLEFEVY 230
QY 457 LEYLQNRFSSEEQAAVQWSTVLIQFLOKRAKNDATITPTTNASLITKLOAQONW 516
Db 231 LEYLQNRFSSEEQAAVQWSTVLIQFLOKRAKNDATITPTTNASLITKLOAQONW 290
QY 517 LQDMTHILIRSFKEFLOSLRALROM 543
Db 291 LQDMTHILIRSFKEFLOSLRALROM 317

RESULT 30
US-08-468-609A-145

Sequence 145, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Capaton, Maïre H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKeatin, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kumman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-609A-145

Query Match 32.7%; Score 935; DB 3; Length 317;
Best Local Similarity 63.0%; Pred. No. 2,1e-69;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;
QY 240 DPHSNSSFYRLRFLRYRAERSKTFTTMYKLOH-----HCVIDAWSGAR 287
Db 24 DPNNINSEMDMLIERNLRTPNILAFVR-AVKHLENASGIEALIRNLQPLPSATAPSR 82
QY 288 HVOGLRAQEEFGCGEWS-----PEAMGTPTWT-ESSSPRAENEVSTPMQALTT 336
Db 83 HPILIIKA-----GDWQEFREKLTFLVLTLEQAOEOOYIEGRISPGG----- 125
QY 337 NKDDNLIIFRDSANATSLPVEFMVPPGEDSKVAAPHROPLTSSRIDKQIRYILDGIS 396
Db 126 -----SGGGSNM-----APVPGEDSKVAAPHROPLTSSRIDKQIRYILDGIS 170
QY 397 ALRKETCNKSNMCESSKEALAEANNLNPKAEKGGCGGSEFNETCLVITLLEFEVY 456
Db 171 ALRKETCNKSNMCESSKEALAEANNLNPKAEKGGCGGSEFNETCLVITLLEFEVY 230
QY 457 LEYLQNRFSSEEQAAVQWSTVLIQFLOKRAKNDATITPTTNASLITKLOAQONW 516


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Qy      420 NUNPKNAEDGCFOSGFNEETCLVYKIIITGLLEFVLEYLONFPESSEEDARAVQNSTK 479
        |||||
Db      61  NUNPKNAEDGCFOSGFNEETCLVYKIIITGLLEFVLEYLONFPESSEEDARAVQNSTK 120
        |||||
Qy      480 VLIQLOKRAKNDAITTPDPTTNASLITKLOAQNQMLQDMTTHILRSFKFPOSSLRA 539
        |||||
Db      121 VLIQLOKRAKNDAITTPDPTTNASLITKLOAQNQMLQDMTTHILRSFKFPOSSLRA 180
        |||||
Qy      540 LRQM 543
        ||||
Db      181 LRQM 184

```

RESULT 35

US-08-567-048-2
; Sequence 2, Application US/08567048

1 GENERAL INFORMATION:
2 APPLICANT: SAVINO, Rocco
3 APPLICANT: LAHM, Armin
4 APPLICANT: CLIBERTO, Gennaro
5 TITLE OF INVENTION: METHOD FOR SELECTING SUPERAAGONISTS,
6 TITLE OF INVENTION: ANTIAGONISTS AND SUPERAAGONISTS FOR HORMONES HAVING
7 TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
8 NUMBER OF SEQUENCES: 15
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: BROWDY AND NEIMARK
11 STREET: 419 Seventh Street, N.W., Suite 300
12 City: Washington
13 STATE: D.C.
14 COUNTRY: USA
15

Query Match	32.6%	Score 934	DB 2:	Length 184;
Best Local Similarity	100.0%	Pred. No.	1.1e-69;	
Matches 184;	Conservative	0;	Mismatches	0;
			Indels	0
			Gaps	0

Qy	Db	Qy	Db
360	1	420	61
PVPPEDESDVAA	PVPPEDESDVAA	NLNLPRKAAKGGC	NLNLPRKAAKGGC
PHRQPLTSSERIDK	PHRQPLTSSERIDK	FGSGFNEETCLYKI	FGSGFNEETCLYKI
IKQRIYILDI	IKQRIYILDI	ITGLLEFEYLYEYL	ITGLLEFEYLYEYL
SAARKETCNMNCES	SAARKETCNMNCES	KLNRPFSSBEQAAV	KLNRPFSSBEQAAV
KELAEEN 419	KELAEEN 60	OMSTK 479	OMSTK 120

Qy	480	VLIQFQOKAKNLDIAITTEDDPTTNSLITKLOAQONQWLODWTTHLIIRSFKEFLOSSLA	539
Db	121	VLIQFQOKAKNLDIAITTEDDPTTNSLITKLOAQONQWLODWTTHLIIRSFKEFLOSSLA	180
Qy	540	LROM 543	
Db	181	LROM 184	

RESULT 36
5186931-1

; Patent No. 5186931
; APPLICANT: KIS

APPLICANT: Kishimoto, Tadamitsu; Hirano, Toshio; Akiyama, Yukio;
Okano, Akira; Matsui, Hiroshi; Takahara, Yoshiyuki
TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
MARROW TRANSPLANTATION
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/366,866
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 81,746
FILING DATE: 05-AUG-1987
SEQ ID NO.:1
LENGTH:184
5186931-1

Query Match 32.6%; Score 934; DB 69; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.1e-69;
 Matches 184; Conservative 0; Indels 0; Gaps 0.

Qy	360	PVPPGDSKDVAAPHROPTSSERIDKQIRYLIDGISMUKETCNKSMCESSKEALAEN	41.9
Db	1	PVPPGDSKDVAAPHROPTSSERIDKQIRYLIDGISMUKETCNKSMCESSKEALAEN	60
Qy	420	NLNLPMKAEDGCFOSGFNEETCLVKIITGLLEFVYLEYLNRFESSEBOARAVONSTK	4.79
Db	61	NLNLPMKAEDGCFOSGFNEETCLVKIITGLLEFVYLEYLNRFESSEBOARAVONSTK	120
Qy	480	VLIQIPLQKAKNLDAITTPDPTTNASLLTKLOAONQMLQDMTTHILIRSFKEFIQSSLR	53.3
Db	121	VLIQIPLQKAKNLDAITTPDPTTNASLLTKLOAONQMLQDMTTHILIRSFKEFIQSSLR	180
Qy	540	LROM 543	
Db	181	LROM 184	

RESULT 37

US-07-632-070B-1.
; Sequence 1, Application US/07632070B
; Patent No. 5264209

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COMPUTER READABLE FORM:
MEDIUM TYPE: Disette, 5.25 inch, 360 Kb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: NBI

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/632,070B
FILING DATE: 19901221
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-32273
FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-222353
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-250460
FILING DATE: 21 SEPT 1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-07-632-070B-1

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPGEDESKDVAAPHROPLTSSERIDKQIRYILIDGISLRKETCNKSNMCESSKEALAEN 419
Db 2 PVPGEDESKDVAAPHROPLTSSERIDKQIRYILIDGISLRKETCNKSNMCESSKEALAEN 61
QY 420 NLNLPKMAEKDGCFOGSEETCLVKIITGLLEFEVYLEYONRFESSSEQARAVOMSTK 479
Db 62 NLNLPKMAEKDGCFOGSEETCLVKIITGLLEFEVYLEYONRFESSSEQARAVOMSTK 121
QY 480 VLIQFLOKAKNLDATTPDPTTNASLITKLOAQONQWLODMTTHLILRSFKEFLQSSIRA 539
Db 122 VLIQFLOKAKNLDATTPDPTTNASLITKLOAQONQWLODMTTHLILRSFKEFLQSSIRA 181
QY 540 LRQM 543
Db 182 LRQM 185

RESULT 38
US-07-918-181A-2
Sequence 2, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-918-181A-2

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPGEDESKDVAAPHROPLTSSERIDKQIRYILIDGISLRKETCNKSNMCESSKEALAEN 419
Db 2 PVPGEDESKDVAAPHROPLTSSERIDKQIRYILIDGISLRKETCNKSNMCESSKEALAEN 61
QY 420 NLNLPKMAEKDGCFOGSEETCLVKIITGLLEFEVYLEYONRFESSSEQARAVOMSTK 479
Db 62 NLNLPKMAEKDGCFOGSEETCLVKIITGLLEFEVYLEYONRFESSSEQARAVOMSTK 121
QY 480 VLIQFLOKAKNLDATTPDPTTNASLITKLOAQONQWLODMTTHLILRSFKEFLQSSIRA 539
Db 122 VLIQFLOKAKNLDATTPDPTTNASLITKLOAQONQWLODMTTHLILRSFKEFLQSSIRA 181
QY 540 LRQM 543
Db 182 LRQM 185

RESULT 39
US-08-231-575-2
Sequence 2, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-575-2

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPPEGDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNCESSKEALAEN 419
| | | | |
DB 2 PVPPEGDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNCESSKEALAEN 61
| | | | |
QY 420 NINLPMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFSSSEQARAAYOMSTK 479
| | | | |
DB 62 NINLPMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFSSSEQARAAYOMSTK 121
| | | | |
QY 480 VLIQFLOKKAKNLDAITTPDPPTTNASLTKLOAONOMLODMTHLILRSFKFELQSSLRA 539
| | | | |
DB 122 VLIQFLOKKAKNLDAITTPDPPTTNASLTKLOAONOMLODMTHLILRSFKFELQSSLRA 181
| | | | |
QY 540 LRQM 543
| | | | |
DB 182 LRQM 185

RESULT 40

US-08-246-427A-5
; Sequence 5, Application US/08246427A
; Patent No. 5641657
; GENERAL INFORMATION:
; APPLICANT: ROSEN, ET AL.
; TITLE OF INVENTION: Interleukin-6 Splice Variant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,427A
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-246-427A-5

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred.No.11e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPPEGDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNCESSKEALAEN 419
| | | | |
DB 2 PVPPEGDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNCESSKEALAEN 61
| | | | |
QY 420 NINLPMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFSSSEQARAAYOMSTK 479
| | | | |
DB 62 NINLPMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFSSSEQARAAYOMSTK 121
| | | | |

QY 480 VLIQFLOKKAKNLDAITTPDPPTTNASLTKLOAONOMLODMTHLILRSFKFELQSSLRA 539
| | | | |
DB 122 VLIQFLOKKAKNLDAITTPDPPTTNASLTKLOAONOMLODMTHLILRSFKFELQSSLRA 181
| | | | |
QY 540 LRQM 543
| | | | |
DB 182 LRQM 185

Search completed: December 9, 2004, 09:22:48
Job time: 56.714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:39:26 ; Search time 210.95 Seconds
(without alignments)
923.396 Million cell updates/sec

Title: US-09-462-416-7
Perfect score: 2861
Sequence: 1 MAAVGCALALAAVGNAL.....LILRSFKPLQSLRALRQM 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: _Geneseq_23sep04: *
2: geneseqp1980s: *
3: geneseqp1980s: *
4: geneseqp2000s: *
5: geneseqp2000s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2861	100.0	543	2	AAV03164
2	2769.5	96.8	570	6	ABP72702
3	2663.5	93.1	515	3	AAAB5404
4	2646	92.5	525	2	AAW36846
5	2512.5	87.8	500	2	AAW36847
6	2149.5	75.1	419	2	AAV30938
7	1921	67.1	592	2	AAW70797
8	1921	67.1	592	3	AAV92185
9	1921	67.1	592	7	ABW02165
10	1918	67.0	468	1	AAV90284
11	1918	67.0	468	2	AAAR37215
12	1918	67.0	468	4	AAAB3655
13	1918	67.0	468	5	AAE28593
14	1918	67.0	468	5	ABW78191
15	1918	67.0	468	5	ABP72697
16	1918	67.0	468	7	ADCO7187
17	1917	67.0	690	3	AAV92195
18	1915.5	67.0	468	3	AAV92196
19	1915	66.9	468	2	AAAR38364
20	1913	66.9	357	6	ABP72699
21	1912	66.8	477	2	AAV92197
22	1910	66.8	360	2	AAW70804
23	1910	66.8	360	3	AAV92199
24	1910	66.8	360	7	ABW02172
25	1910	66.8	468	1	AAV90525

26	1907	66.7	364	6	ABP72698	Abp72698 Soluble i
27	1900	66.4	468	2	AAW71371	AAW71371 Human int
28	1858	64.9	345	3	AAV55071	AAV55071 SR345 pro
29	1852	64.7	344	1	AAV90528	AAV90528 B cell bc
30	1788	62.5	1158	3	AAV92205	AAV92205 Fusion po
31	1788	62.5	1158	7	ABW02178	ABW02178 Human cyt
32	1783	62.3	1168	3	AAV92204	AAV92204 Fusion po
33	1783	62.3	1168	7	ABW02177	ABW02177 Human cyt
34	1763	61.6	325	7	AAO23014	AAO23014 Human int
35	1759	61.5	1042	2	AAV70122	AAV70122 IL8-R typ
36	1757	61.4	325	2	AAO23016	AAO23016 Human int
37	1754	61.3	325	7	AAO23018	AAO23018 Human int
38	1748	61.1	325	3	AAV53389	AAV53389 Human int
39	1748	61.1	325	3	AAV53390	AAV53390 Bovine in
40	1748	61.1	325	7	AAO23015	AAO23015 Human int
41	1742	60.9	325	7	AAO23017	AAO23017 Human int
42	1715	59.9	323	1	AAV90527	AAV90527 B cell bc
43	1683	58.8	315	2	AAW70805	AAW70805 Amino aci
44	1683	58.8	315	3	AAV92200	AAV92200 Soluble h
45	1683	58.8	315	7	ABW02173	ABW02173 Human IL-

ALIGNMENTS

RESULT 1
ID AAY03164 standard; protein; 543 AA.
XX
AC AAY03164;
XX
DT 11-JUN-1999 (first entry)
XX
DE Chimeric sIL-6R/IL-6 protein.
XX
XX Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; IL-6/IL-6;
KW chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
KW human haematopoietic cell; bone marrow transplantation; mammalian cancer;
KW hepatotoxic agent protection; haematopoiesis; liver disorder;
KW neurological disorder.
XX
OS Synthetic.
XX
PN WO9902552-A2.
XX
PD 21-JAN-1999.
XX
PF 09-JUL-1998; 98WO-IL000321.
XX
PR 10-JUL-1997; 97IL-00121284.
PR 30-DEC-1997; 97IL-00122818.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Revel M, Chebach J, Lapidot T, Kollet O;
XX
XX WPI, 1999-120776/10.
XX
XX New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.
PT treating cancers, bone marrow transplantation, increasing haematopoiesis
PT or treating liver or neurological disorders.
XX
PS Claim 6; Fig 3; 77bp; English.
XX
XX This sequence represents the chimeric glycosylated soluble interleukin-6
CC receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the
CC invention. It comprises a fusion protein product between all of the
CC naturally occurring form of sIL-6R and all of the naturally occurring
CC form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a
CC similar fashion to the glycosylation of naturally occurring sIL-6R and IL
CC -6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of
CC highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo

CC engraftment of human haematopoietic cells in bone marrow transplantation
 CC and protecting liver from hepatotoxic agents. They can be used for the
 CC preparation of a medicament for treating mammalian cancers by way of
 CC inhibition of cancer cells, for enhancement of bone marrow
 CC transplantation by way of eliciting engraftment of human haematopoietic
 CC cells in bone marrow transplantation, for increasing haematopoiesis, for
 CC treating liver or neurological disorders, or in other applications in
 CC which IL-6 or siL-6R are used

XX
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2861; DB 2; Length 543;
 Best Local Similarity 100.0%; Pred. No. 4.2e-183;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIAVGALLAALIAAPGALAPRRCPAQRVAVRGVLTSLPGDSVTLTCTPGVPEEDNATVHW 60
 DB 1 MIAVGALLAALIAAPGALAPRRCPAQRVAVRGVLTSLPGDSVTLTCTPGVPEEDNATVHW 60
 QY 61 VLKRPAGSHPSRMAGMGRLLLRSLVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRLLLRSLVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFRKSPISNVVCEMGPRSTPSLTTRKAVILVRKFQNSPAEDFQEPQYQSQESQKFSQCLAV 180
 DB 121 CFRKSPISNVVCEMGPRSTPSLTTRKAVILVRKFQNSPAEDFQEPQYQSQESQKFSQCLAV 180
 QY 181 PEGGSSFYIVSMCVASSVSGSKFSTKTFQGGIILQPPPPANITVTVAARNRMLSVTWQD 240
 DB 181 PEGGSSFYIVSMCVASSVSGSKFSTKTFQGGIILQPPPPANITVTVAARNRMLSVTWQD 240
 QY 241 PHSNSSFYRLRPELRYARSRKSTFTTWVYKDLQHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 DB 241 PHSNSSFYRLRPELRYARSRKSTFTTWVYKDLQHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 QY 301 GEMSENPAMGTWTSRSRPPANEVSTWQALTTNKDDNILLFRDSANATSLPVEFMP 360
 DB 301 GEMSENPAMGTWTSRSRPPANEVSTWQALTTNKDDNILLFRDSANATSLPVEFMP 360
 QY 361 VPGEBSKVDAAPRRKOPLTSSERIDKQIRYILDGISALRKETCKSMKSCSSKEALAEEN 420
 DB 361 VPGEBSKVDAAPRRKOPLTSSERIDKQIRYILDGISALRKETCKSMKSCSSKEALAEEN 420
 QY 421 LNP.PKMAEKDGCFOSGFNEETCLVKIITGLLEFVYLEYLQNFPESEEQARAQVOMSTKV 480
 DB 421 LNP.PKMAEKDGCFOSGFNEETCLVKIITGLLEFVYLEYLQNFPESEEQARAQVOMSTKV 480
 QY 481 LIQFLQKAKNLDALITPPTNANSLITKLOAQONQIQLDMTTHILRSFKEPLQSSIRAL 540
 DB 481 LIQFLQKAKNLDALITPPTNANSLITKLOAQONQIQLDMTTHILRSFKEPLQSSIRAL 540
 QY 541 ROM 543
 DB 541 ROM 543

RESULT 2
 ABP72702
 ID ABP72702 standard; protein: 570 AA.
 AC ABP72702;
 XX
 XX

DT 11-JUN-2003 (first entry)
 XX Human interleukin-6-receptor isoform DS-siL-6R fusion protein.
 DE Human interleukin-6; receptor; DS-siL-6R; antibacterial; virucide;
 XX anti-HIV; antineumatic; antiarthritic; antiinflammatory;
 KW immunosuppressive; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FH Protein 1..364 DS-siL-6R
 FT Peptide /label=.376
 FT Peptide /label=.376
 FT Protein 377..560
 FT Peptide /label=IL-6
 FT Peptide 561..570
 FT /label=C-myc tag

PN WO2003014359-A2.
 XX 20-FEB-2003.
 XX

PF 02-AUG-2002; 2002WO-GB003581.
 XX
 XX
 PR 03-AUG-2001; 2001GB-00019015.
 XX

PA (UYCA-) UNIV COLLEGE CARDIFF.
 XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
 PA

XX Jones SA, Topley N;
 XX WPI; 2003-256588/25.
 XX

PT New fusion protein having a functional IL-6 and DS-siL-6R molecule,
 PT useful for the manufacture of a medicament for the prophylaxis or
 PT treatment of an infectious disease, and an inflammatory or immunological
 PT disorder.
 PT

XX Disclosure; Fig 5; 46pp; English.
 XX

CC The present sequence is the protein sequence of a novel fusion protein
 CC comprising a soluble form of the human interleukin-6 receptor, denoted DS
 CC -siL-6R (see also ABP72698), joined via a peptide linker to a human IL-6
 CC molecule (see also ABP72700), with a C-terminal c-myc tag sequence.
 CC Administration of this fusion protein results in the increased expression
 CC of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. High levels of
 CC MIP-1alpha, MIP-1beta and RANTES complete with HIV for binding to CCR5
 CC and effectively suppress HIV entry. The fusion protein can be used in the
 CC treatment of any disease in which the infectious agent binds to CCR5,
 CC especially M-trophic strains of HIV. The invention also provides a
 CC nucleic acid molecule encoding the fusion protein, an expression vector,
 CC a host cell, and a method of producing the fusion protein in the host
 CC cell. The fusion protein, nucleic acid or vector can be used in the
 CC manufacture of a medicament for the prophylaxis or treatment of an
 CC infectious disease (especially AIDS caused by a M-trophic strain of HIV,
 CC or bacterial peritonitis), an inflammatory disorder or an immunological
 CC disorder (especially rheumatoid arthritis), when it is desirable to
 CC increase or resolve an immune response (claimed)
 CC
 XX
 SQ Sequence 570 AA;

Query Match 96.8%; Score 2769.5; DB 6; Length 570;
 Best Local Similarity 95.4%; Pred. No. 6e-177;
 Matches 536; Conservative 0; Mismatches 5; Indels 21; Gaps 4;

QY 1 MIAVGALLAALIAAPGALAPRRCPAQRVAVRGVLTSLPGDSVTLTCTPGVPEEDNATVHW 60
 DB 1 MIAVGALLAALIAAPGALAPRRCPAQRVAVRGVLTSLPGDSVTLTCTPGVPEEDNATVHW 60
 QY 61 VLKRPAGSHPSRMAGMGRLLLRSLVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRLLLRSLVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFRKSPISNVVCEMGPRSTPSLTTRKAVILVRKFQNSPAEDFQEPQYQSQESQKFSQCLAV 179
 DB 121 CFRKSPISNVVCEMGPRSTPSLTTRKAVILVRKFQNSPAEDFQEPQYQSQESQKFSQCLAV 179
 QY 180 PEGGSSFYIVSMCVASSVSGSKFSTKTFQGGIILQPPPPANITVTVAARNRMLSVTWQD 239
 DB 180 PEGGSSFYIVSMCVASSVSGSKFSTKTFQGGIILQPPPPANITVTVAARNRMLSVTWQD 238

```

QY 240 DPHSNNSFYRLRPELRVRAERSKFTETMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFG 299
DB 239 DPHSNNSFYRLRPELRVRAERSKFTETMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFG 298
QY 300 QGEMSWSPBAMGTPWTSRSPPAENSVSTPMQALTTNKDDNLLFRDSANATSLP---- 355
DB 299 QGEMSWSPBAMGTPWTSRSPPAENSVSTPMQALTTNKDDNLLFRDSANATSLP----- 358
QY 356 -----VFMPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDIISALRKE 401
DB 359 RSCSGIGGGGGGGGSLPEVPPGEDSKDVAAPHROPLTSSERTDKQIRYILDIISALRKE 418
QY 402 TCNKSNNKSSKEALANNLNLPMKAEKDGCFQSGFNEETCLVKIITGLLEFEVLEYIQ 461
DB 419 TCNKSNNKSSKEALANNLNLPMKAEKDGCFQSGFNEETCLVKIITGLLEFEVLEYIQ 478
QY 462 NRESESEQARAVQWSTKVLIOFLQKAKNLDAITTPPTTNASLLTKLQANQWLODMT 521
DB 479 NRESESEQARAVQWSTKVLIOFLQKAKNLDAITTPPTTNASLLTKLQANQWLODMT 538
QY 522 THILRSFKFLOSSLRALRQM 543
DB 539 THILRSFKFLOSSLRALRQM 560

RESULT 3
AAB15404
ID AAB15404 standard; protein; 515 AA.
AC AAB15404;
XX
XX 17-JAN-2001 (first entry)
DE IL-6R/IL-6 fusion protein.
XX
XX Fusion protein; human; interleukin 6 receptor; Pichia pastoris; yeast;
XX drug; myeloid stem cell; platelet; blood.
XX
XX Homo sapiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 57 /note= "encoded by GGC"
FT Misc-difference 281 /note= "encoded by CAA"
FT Misc-difference 281 /note= "encoded by CAA"
PN JP200016539-A.
XX
XX 20-JUN-2000.
XX
XX 03-DEC-1998; 98JP-00343933.
XX
XX 03-DEC-1998; 98JP-00343933.
XX
XX (TOYO) TOSOH CORP.
XX
XX WPI; 2000-485548/43.
XX
XX N-PSDB; AAA70763.
XX
XX Yeast of Pichia pastoris genus transformed by expression vector
XX containing gene encoding fused protein of interleukin-6 receptor (IL-6R)
XX protein for amplifying myeloid stem cells and increasing platelets.
XX
XX Example 1; Page 8-10; 11pp; Japanese.
XX
XX The invention relates to the production of a fusion protein comprising
XX the human interleukin 6 receptor (IL-6R) fused to the human IL-6 protein
XX in a Pichia pastoris yeast cell. This sequence represents the IL-6R/IL-6
XX fusion protein. The coding sequence for this protein is cloned into an
XX expression vector for introduction into P. pastoris. The IL-6R protein is
XX used as a drug for amplifying myeloid stem cells and increasing platelets
XX
XX

```

```

CC In blood
XX
XX Sequence 515 AA;
SQ
Query Match 93.1%; Score 2663.5; DB 3; Length 515;
Best Local Similarity 96.8%; Pred. No. 6,6e-170;
Matches 507; Conservative 1; Mismatches 7; Indels 9; Gaps 1;

QY 20 LAPRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHWLRKPAAGSHSRMAGMR 79
DB 1 LAPRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHWLRKPAAGSHSRMAGMR 60
QY 80 RLILRSVQLHDSGNVSCYRAGRAGTVHLLVVPPEPQLSCFRKSPLSNVVCEMPRST 139
DB 61 RLILRSVQLHDSGNVSCYRAGRAGTVHLLVVPPEPQLSCFRKSPLSNVVCEMPRST 120
QY 140 PSLITKAVLLVRKFNQSPADPFOEPCQYQESQKFSQCLAVPEGDSFFIYVSCVASSVG 199
DB 121 PSLITKAVLLVRKFNQSPADPFOEPCQYQESQKFSQCLAVPEGDSFFIYVSCVASSVG 180
QY 200 SKFSKTQTFQGGGIIQDPDPANITVAVARNRMLSVTWQDPHSNNSFYRLRPELRVRA 259
DB 181 SKFSKTQTFQGGGIIQDPDPANITVAVARNRMLSVTWQDPHSNNSFYRLRPELRVRA 240
QY 260 ERSKTFETMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGGEMSWSPBAMGTPWTSR 319
DB 241 ERSKTFETMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGGEMSWSPBAMGTPWTSR 300
QY 320 SPPAENSVSTPMQALTTNKDDNLLFRDSANATSLPVEBMPVPPGEDSKDVAAPHROPLT 379
DB 301 SPPAENSVSTPMQALTTNKDDNLLSELY-----APVPPGEDSKDVAAPHROPLT 351
QY 380 SSERIDKQIRYILDIISALRKETCNKSNKSSKEALANNLNLPMKAEKDGCFQSGFNE 439
DB 352 SSERIDKQIRYILDIISALRKETCNKSNKSSKEALANNLNLPMKAEKDGCFQSGFNE 411
QY 440 ETCVLKIIIGLLEFEVLEYLQNRFESESEQARAVQWSTKVLIOFLQKAKNLDAITTPD 499
DB 412 ETCVLKIIIGLLEFEVLEYLQNRFESESEQARAVQWSTKVLIOFLQKAKNLDAITTPD 471
QY 500 PTTNASLLTKLQANQWLODMTTHILRSFKFLOSSLRALRQM 543
DB 472 PTTNASLLTKLQANQWLODMTTHILRSFKFLOSSLRALRQM 515

RESULT 4
AAM36846
ID AAM36846 standard; protein; 525 AA.
AC AAM36846;
XX
XX 25-MAR-2003 (revised)
XX
XX 25-MAR-1998 (first entry)
XX
XX Human fusion polypeptide H-IL-6 with 18 amino acid linker.
XX
XX Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
XX protein interaction; therapeutic; antagonist.
XX
XX Synthetic.
OS Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..19 /label= signal_peptide
FT Protein 20..524 /note= "H-IL-6 fusion polypeptide"
FT Region 324..341 /label= linker region
FT /note= "links together COOH-terminus of sIL-6R with the
XX NH2-terminus of IL-6"
XX
XX MO9732891-A2.

```

XX 12-SEP-1997.
 PD 07-MAR-1997; 97WO-DE000458.
 XX 07-MAR-1996; 96DE-01008813.
 XX (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PA Rosejohn S;
 PI WPI; 1997-470536/43.
 XX N-PSDB; AAT97848.
 DR Conjugate of two peptide(s) with mutual affinity connected by a linker -
 XX used to modulate interactions between proteins, e.g. for ex vivo
 PT expansion of human stem cells.
 XX Disclosure; Fig 1; 19pp; German.
 PS This sequence represents the fusion polypeptide H-IL-6 which contains an
 XX 18 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX Sequence 525 AA;
 SQ
 Query Match 92.5%; Score 2646; DB 2; Length 525;
 Best Local Similarity 93.7%; Pred. No. 1e-168;
 Matches 509; Conservative 2; Mismatches 14; Indels 18; Gaps 2;
 QY 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 DB 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 QY 61 VLKRPAGSHPRMAGRRLLRSVOLHDSGNVSCVRRARPAGTVALLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPRMAGRRLLRSVOLHDSGNVSCVRRARPAGTVALLVDVPEEPQLS 120
 QY 121 CPERKPLSNVVCCEWGPSTSLTTKAVLVKRFQNSPAEDFOBPCCQYSQSKFSCQLAV 180
 DB 121 CPERKPLSNVVCCEWGPSTSLTTKAVLVKRFQNSPAEDFOBPCCQYSQSKFSCQLAV 180
 QY 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 DB 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 QY 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 DB 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 QY 241 PHMNSGFYLRPELRARERSKFTTMMWKDLOHCHVIDHANSGLRHVVQLPAQSEFQ 300
 DB 241 PHMNSGFYLRPELRARERSKFTTMMWKDLOHCHVIDHANSGLRHVVQLPAQSEFQ 300
 QY 301 GEWSEMSPEAMGTPTWESRSPPAENEVSPTMALTTNKDDNITFRDSANATSLPYEFMP 360
 DB 301 GEWSEMSPEAMGTPTWESRSPPAENEVSPTMALTTNKDDNITFRDSANATSLPYEFMP 360
 QY 361 VPPGSESKDVAARHROPITSSERIDKQIRIYLDGISALRKETKNKSNMCESSKEALAENN 420
 DB 361 VPPGSESKDVAARHROPITSSERIDKQIRIYLDGISALRKETKNKSNMCESSKEALAENN 420
 QY 421 LNLPRKAEKDCQSGFNEETCLVKIITGLLEFEVLEYLQNFESSEBOARAVOMSTVY 480
 DB 421 LNLPRKAEKDCQSGFNEETCLVKIITGLLEFEVLEYLQNFESSEBOARAVOMSTVY 480
 QY 481 LLIQFLOKAKNDAITTPPTTNASILLTKLQAOQNLQDMTTHLLIRSFKEFLQSSIRAL 540
 DB 481 LLIQFLOKAKNDAITTPPTTNASILLTKLQAOQNLQDMTTHLLIRSFKEFLQSSIRAL 540
 QY 540 LLIQFLOKAKNDAITTPPTTNASILLTKLQAOQNLQDMTTHLLIRSFKEFLQSSIRAL 540
 DB 540 LLIQFLOKAKNDAITTPPTTNASILLTKLQAOQNLQDMTTHLLIRSFKEFLQSSIRAL 540

QY 541 ROM 543
 DB 523 ROM 525
 RESULT 5
 AAM36847
 ID AAM36847 standard; protein; 500 AA.
 AC AAM36847;
 XX 25-MAR-2003 (revised)
 DT 25-MAR-1998 (first entry)
 XX Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 DE Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 XX protein interaction; therapeutic; antagonist.
 XX Synthetic.
 OS Homo sapiens.
 OS Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..500
 FT /note= "H-IL-6 fusion polypeptide"
 FT Region 304..316
 FT /label= linker region
 FT /note= "Links together COOH-terminus of sIL-6R with the
 FT NH2-terminus of IL-6"
 XX MO9732891-A2.
 XX 12-SEP-1997.
 PD 07-MAR-1997; 97WO-DE000458.
 XX 07-MAR-1996; 96DE-01008813.
 XX (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PA Rosejohn S;
 PI WPI; 1997-470536/43.
 XX N-PSDB; AAT97849.
 DR Conjugate of two peptide(s) with mutual affinity connected by a linker -
 XX used to modulate interactions between proteins, e.g. for ex vivo
 PT expansion of human stem cells.
 XX Disclosure; Fig 2; 19pp; German.
 PS This sequence represents the fusion polypeptide H-IL-6 which contains an
 XX 13 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX Sequence 500 AA;
 SQ
 Query Match 87.8%; Score 2512.5; DB 2; Length 500;
 Best Local Similarity 90.1%; Pred. No. 8.3e-160;
 Matches 489; Conservative 1; Mismatches 10; Indels 43; Gaps 3;
 QY 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 DB 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60


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QY 61 VLKRAAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQIS 120
DB 61 VLKRAAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQIS 120
QY 121 CRRKSPLSNVCEWGPSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
DB 121 CRRKSPLSNVCEWGPSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGIIQDPDPANITVTAVARNPRLSTVMQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGIIQDPDPANITVTAVARNPRLSTVMQD 240
QY 241 PHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVOLRAQEFQ 300
DB 241 PHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVOLRAQEFQ 300
QY 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLPYEFMP 360
DB 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLPYEFMP 360
QY 361 VPPGDSKVVAAPHROPULTSSERIDKQIRIYILDGIALRKETCNKSNMCESSKEALAENK 420
DB 361 VPPGDSKVVAAPHROPULTSSERIDKQIRIYILDGIALRKETCNKSNMCESSKEALAENK 420
QY 421 LNLPRKAEKDCGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESEBOARAVOMSTKY 480
DB 421 LNLPRKAEKDCGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESEBOARAVOMSTKY 480
QY 481 LIQFLQKKAKNLDAITTPDPTNASLITKLQAOQWLODMTTHLILRSFKFELQSSLRAL 540
DB 481 LIQFLQKKAKNLDAITTPDPTNASLITKLQAOQWLODMTTHLILRSFKFELQSSLRAL 540
QY 541 ROM 543
DB 541 ROM 543
QY 498 ROM 500
DB 498 ROM 500

```

RESULT 6
AA30938
ID AAY30938 standard; protein; 419 AA.

AC AAY30938;
XX
DT 19-OCT-1999 (first entry)
XX
DE Human IL-6 receptor/IL-6 fusion protein.
XX
KW IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
XX stem cell; platelet; reduced antigenicity.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT 1..420
FT /note="No start codon given"
FT
XX JP11196867-A.
XX
XX 27-JUL-1999.
XX
XX 09-JAN-1998; 98JP-00002921.
XX
XX 09-JAN-1998; 98JP-00002921.
XX
XX (TOYO) TOSOH CORP.
XX
XX
XX MPI: 1999-496648/42.
XX
XX N-PSDB; AA209202.
XX
XX
XX New interleukin-6 receptor-interleukin-6 fused protein and gene - used
XX for growth of bone marrow stem cells and platelets.
XX
XX

```

XX  
PS Example 1; Page 5-8; 8pp; Japanese.  
XX  
CC This invention describes a novel gene which encodes a fusion protein of  
CC interleukin-6 (IL-6) receptor and bound with a gene sequence encoding for  
CC IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding  
CC protein has applications for the growth of bone marrow stem cells and  
CC platelets. Transmission of a signal of IL-6 to target cells for  
CC stimulation with reduced antigenicity is possible. This sequence  
CC represents the IL-6 receptor/IL-6 fusion protein described in the  
CC invention  
XX  
XX Sequence 419 AA;  
XX  
Query Match 75.1%; Score 2149.5; DB 2; Length 419;  
Best Local Similarity 95.8%; Pred. No. 1.4e-135;  
Matches 410; Conservative 3; Mismatches 6; Indels 9; Gaps 1;  
QY 116 EPQLSCFRKSPLSNVCEWGPSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFS 175  
DB 1 EPQLSCFRKSPLSNVCEWGPSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFS 60  
QY 176 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTFQCGGIIQDPDPANITVTAVARNPRLS 235  
DB 61 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTFQCGGIIQDPDPANITVTAVARNPRLS 120  
QY 236 VTMQDPHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVOLRAQ 295  
DB 121 VTMQDPHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVOLRAQ 180  
QY 296 BEFGQGEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLP 355  
DB 181 BEFGQGEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILSELV----- 234  
QY 356 VERMPVPPGEDSKDVAAPHROPULTSSERIDKQIRIYILDGIALRKETCNKSNMCESSKEA 415  
DB 235 ---APVPPGEDSKDVAAPHROPULTSSERIDKQIRIYILDGIALRKETCNKSNMCESSKEA 291  
QY 416 LAENNINLPRKAEKDCGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESEBOARAVO 475  
DB 292 LAENNINLPRKAEKDCGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESEBOARAVO 351  
QY 476 MSTKVLIQFLQKKAKNLDAITTPDPTNASLITKLQAOQWLODMTTHLILRSFKFELQSS 535  
DB 352 MSTKVLIQFLQKKAKNLDAITTPDPTNASLITKLQAOQWLODMTTHLILRSFKFELQSS 411  
QY 536 SUPALROM 543  
DB 412 SUPALROM 419

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RESULT 7
AAW70797
ID AAW70797 standard; protein; 592 AA.

AC AAW70797;
XX
DT 03-FEB-1999 (first entry)
XX
DE Human interleukin-6R-alpha-Fc.
XX
XX
XX gp130; cytokine antagonist; interleukin; gamma-interferon;
XX granulocyte macrophage colony-stimulating factor; J peptide;
XX transforming growth factor-beta.
XX
XX Synthetic.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..358
FT /note="human IL-R-alpha"
FT Peptide 1..19
FT /note="signal peptide"
FT

```

FT Misc-difference 2
FT /label= L2V
FT /note= "changed to accomodate a Kozak sequence"
FT Misc-difference 359..360
FT /note= "Ala-Gly bridge"
FT Protein
FT 361..592
FT /note= "Fc domain of human IgG1"
FT Disulfide-bond 371..374
FT
XX US5844099-A.
XX
XX 01-DEC-1998.
XX
XX 27-NOV-1995; 95US-00563105.
XX
XX 20-OCT-1993; 93US-00140222.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Yancopoulos GD, Stahl N, Economides A;
XX
XX WPI; 1999-044669/04.
XX
XX Cytokine antagonists - comprising extracellular domains of specificity-
XX determining and signal-transducing components of cytokine receptor.
XX
XX Example 3; Fig 5; 46pp; English.
XX
XX The present sequence represents the amino acid sequence of human
XX interleukin (IL)-6R-alpha-Fc. The protein is used in the course of the
XX invention. The specification describes cytokine antagonists comprising
XX only the extracellular domain of the specificity-determining component of
XX the cytokine receptor and the extracellular domain of a signal-
XX transducing component of the cytokine receptor. The cytokine is an
XX interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte
XX macrophage colony-stimulating factor (GM-CSF), gamma-interferon or
XX transforming growth factor-beta (TGF-beta). The antagonist is capable of
XX binding the cytokine to form a nonfunctional complex. The compounds have
XX therapeutic activity as cytokine antagonists and can also be used in
XX assays for identifying novel agonists and antagonists of cytokines
XX
XX Sequence 592 AA;
XX
XX Query Match 67.1%; Score 1921; DB 2; Length 592;
XX Best Local Similarity 77.1%; Pred. No. 4.2e-120; Indels 46; Gaps 5;
XX Matches 377; Conservative 22; Mismatches 44;
XX
XX 1 MLAVGCLLAALLAALPAGALAPRRCPADEVARGVLTSLPGDSVLTTCPEVEPEDNATVHM 60
XX 1 MVAVGCLLAALLAALPAGALAPRRCPADEVARGVLTSLPGDSVLTTCPEVEPEDNATVHM 60
XX
XX 61 VLKPPAAGSHPSRWAGKRRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDPPEEPOLS 120
XX 61 VLKPPAAGSHPSRWAGKRRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDPPEEPOLS 120
XX
XX 121 CPEKSPISNVVCEMGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
XX 121 CPEKSPISNVVCEMGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
XX
XX 181 PEGDSSFYIVSMCVASSVSGSKFKTQTFQCGILQDPDPANITVTVANRPRLSTVMD 240
XX 181 PEGDSSFYIVSMCVASSVSGSKFKTQTFQCGILQDPDPANITVTVANRPRLSTVMD 240
XX
XX 241 PHSNNSFYRLRFLRLRARSKFTFTWVKDLOHNVHDAMSGLRHVQVLAQSEFQ 300
XX 241 PHSNNSFYRLRFLRLRARSKFTFTWVKDLOHNVHDAMSGLRHVQVLAQSEFQ 300
XX
XX 301 GEMSEMPPEAMGTWTSRSPPAENEVSTPQALTTNKDDNILLFRDSANATSLPVEFNP 360
XX 301 GEMSEMPPEAMGTWTSRSPPAENEVSTPQALTTNKDDNILLFRDSANATSLPVEFNP 360
XX
XX 361 VPPGDSKVAAPIHROPILTSSERIDKQIRYILDDISALRKETCNKSMCE--SSKEALAE 418
XX 361 VPPGDSKVAAPIHROPILTSSERIDKQIRYILDDISALRKETCNKSMCE--SSKEALAE 418

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DB 358 -----DAGEP-----KSCDKTHGPCPCAPPELLCG 382
QY 419 NNILNLPMAEKDCFGSGFNEETLVKILT---GLTFEVEYLEYLDQ---NRFESSEQAR 472
DB 383 PSVFLPPEPKRDTLMTSRPEVTGVVDVSHEDPEVKFMVYDGVVHNAKTPRREQYN 442
QY 473 AVQMSKVL 481
DB 443 STRVSVVL 451
DB
RESULT 8
AA92185
ID AAY92185 standard; protein; 592 AA.
XX
XX AAY92185;
XX
XX 01-AUG-2000 (first entry)
XX
XX Human IL-6R-alpha-Fc fusion protein.
XX
XX IL-6R-alpha-Fc; cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytostatic; immunomodulator; osteopathic.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..358
XX /label= IL-6R-alpha
XX Peptide 1..19
XX /label= signal peptide
XX Peptide 359..360
XX /note= "Ala-Gly bridge"
XX Protein 361..592
XX /label= IgG1_Fc domain
XX Disulfide-bond 371
XX /note= "Forms inter-chain disulfide bridge that link two
XX Fc domains"
XX Disulfide-bond 374
XX /note= "Forms inter-chain disulfide bridge that link two
XX Fc domains"
XX
XX W020018932-A2.
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99WO-US022045.
XX
XX 25-SEP-1998; 98US-0101658P.
XX 19-MAY-1999; 99US-00313942.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX
XX WPI; 2000-293165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases or
XX disorders encodes a fusion polypeptide capable of binding a cytokine to
XX form a nonfunctional complex.
XX
XX Example 3; Fig 5; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the
XX soluble alpha specificity determining component of the receptor (SR-
XX alpha) and the extracellular domain of the first beta signal transducing
XX component of the cytokine receptor (beta-1) are combined to form
XX heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by

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binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (cellary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia

Sequence 592 AA;

Query Match 67.1%; Score 1921; DB 3; Length 592;
Best Local Similarity 77.1%; Pred. No. 4,2e-120;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

1 MLAVGALIAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
1 MVAVGALIAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
61 VLRKPAAGSHPRMAGMRRLILRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
61 VLRKPAAGSHPRMAGMRRLILRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLLVRKFQNSPADFPQPCQYSGESQKFSQCLAV 180
121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLLVRKFQNSPADFPQPCQYSGESQKFSQCLAV 180
181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIQDPDPANITVTAANPRLSTVWQD 240
181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIQDPDPANITVTAANPRLSTVWQD 240
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
361 VPPGEDSKDVAAPHROPITSSERIDKQIRYIILDGISALRKETCNKSNMCE--SSKEALAE 418
361 VPPGEDSKDVAAPHROPITSSERIDKQIRYIILDGISALRKETCNKSNMCE--SSKEALAE 418
419 NNUNLPKAKKQCGFSGNEETCLVKIIT--GLLEFVYLEYLO--NRFSSEQAR 472
419 NNUNLPKAKKQCGFSGNEETCLVKIIT--GLLEFVYLEYLO--NRFSSEQAR 472
473 AVQWSTKVL 481
473 AVQWSTKVL 481
443 STYRRVSVL 451
443 STYRRVSVL 451

RESULT 9
ABW02165
ID ABW02165 standard; protein; 592 AA.

ABW02165;
12-FEB-2004 (first entry)
Human IL-6Ralpha-Fc protein.
Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
cancer; cachexia; arthritis; cyostatic; osteopathic; therapy; human.

OS Homo sapiens.

XX Key location/Qualifiers
XX Peptide 1..19
XX Protein /label= Signal_peptide
XX Region /note= "Human mature IL-6Ralpha-Fc protein"
XX Domain /note= "Ala-Gly bridge"
XX Disulfide-bond /note= "Human IgG1 Fc domain"
XX Disulfide-bond /note= "Inter-chain disulphide bridge"

US2003143697-A1.
31-JUL-2003.
28-OCT-2002; 2002US-00282162.

22-SEP-1999; 99WO-US022045.
22-MAR-2001; 2001US-00787835.

(STAH/) STAHL N.
(YANC/) YANCOPOULOS G D.
Stahl N, Yancopoulos GD.
WPI; 2003-851784/79.

New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis, or osteoporosis.

Example 3; Fig 5; 300pp; English.

The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors and for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human IL-6Ralpha-Fc protein

Sequence 592 AA;

Query Match 67.1%; Score 1921; DB 7; Length 592;
Best Local Similarity 77.1%; Pred. No. 4,2e-120;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

1 MLAVGALIAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
1 MVAVGALIAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
61 VLRKPAAGSHPRMAGMRRLILRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
61 VLRKPAAGSHPRMAGMRRLILRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLLVRKFQNSPADFPQPCQYSGESQKFSQCLAV 180
121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLLVRKFQNSPADFPQPCQYSGESQKFSQCLAV 180
181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIQDPDPANITVTAANPRLSTVWQD 240
181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIQDPDPANITVTAANPRLSTVWQD 240
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360

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QY 361 VPEGEDSKVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCE--SSKEALAE 418
Db 358 -----DAGEP-----KSCDKTHICTPCCPAPELLGG 382
QY 419 NINLPRKMEKDCFCFSGFNEETCLVKIT---GLLFEVYLEYLQ---NRPESSEEQAR 472
Db 383 PSYFLPEPPKCDLTMTSKRTEPVTGVVDVSHDEPEVKFMWYDGVENVNAKTKPREEQYN 442
QY 473 AVQMSTKVL 481
Db 443 STYRVVSVL 451

RESULT 10
AAP90284
ID AAP90284 standard; protein; 468 AA.
XX
AC AAP90284;
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1992 (first entry)
XX
DE Sequence of a receptor protein for human B cell stimulating factor-2
DE (BSF2 receptor).
XX
KM B cell; immune disorder; therapy; diagnosis; prophylaxis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 2..22
FT /label= hydrophobic region
FT Region 362..386
FT /label= hydrophobic region
FT
FT EP325474-A.
XX
PN 26-JUL-1989.
XX
PD 20-JAN-1989; 89EP-00300536.
XX
PR 22-JAN-1988; 88JP-00012387.
XX
PR 25-JAN-1988; 88JP-00012599.
XX
PR 04-AUG-1988; 88JP-00194885.
XX
PR 14-JAN-1989; 89JP-00007461.
XX
XX
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T.
XX
DR WPI; 1989-214667/30.
XX
DR N-PSDB; AAN90340.
XX
PT Receptor protein for human B cell stimulating factor-2 - obtd. by
PT recombinant DNA techniques and used as diagnostic prophylactic or
PT therapeutic agent.
XX
PS Claim 2; Page 19-21; 63pp; English.
XX
CC The cDNA in AAN90340 was derived from monocyte cell line U937. Isolated
CC BSF2 receptor and DNA encoding it are claimed, as are (b) expression
CC vectors; (c) host organisms; (d) antibodies; and (e) hybridomas. (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 1; Length 468;
Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

1 MLAVGCALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
|||||

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Db 1 MLAVGCALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
QY 61 VLRRPAAGSHPSRWAGMRLLIRSVQLHDSGNYSCYRAGRAGVTHLVDPPEEPQLS 120
Db 61 VLRRPAAGSHPSRWAGMRLLIRSVQLHDSGNYSCYRAGRAGVTHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVNVCWGRPSPTSLTTKAVLLVRKFONSPAEDFOEPCQYSGESQKFSQCLAV 180
Db 121 CFRKSPLSNVNVCWGRPSPTSLTTKAVLLVRKFONSPAEDFOEPCQYSGESQKFSQCLAV 180
QY 181 PEGDSEFYIVSMCVASSVSGSKFSTQTFQCCGILQDPDPANITVTAVANPRMLSTYMQD 240
Db 181 PEGDSEFYIVSMCVASSVSGSKFSTQTFQCCGILQDPDPANITVTAVANPRMLSTYMQD 240
QY 241 PHSWNSFYRLRPELRARYARSKTFTTWVYKDIQHHCVIHDAWSGLRHVVQLRAQEEFQ 300
Db 241 PHSWNSFYRLRPELRARYARSKTFTTWVYKDIQHHCVIHDAWSGLRHVVQLRAQEEFQ 300
QY 301 GEMSEWSPFAMGTPTWTSRSPPAENEVSTPMQALTTKDDNLLFRDSANATSLPVEFMP 360
Db 301 GEMSEWSPFAMGTPTWTSRSPPAENEVSTPMQALTTKDDNLLFRDSANATSLPVEFMP 360
QY 361 VPEGEDSKVAAP 373
Db 357 ----QDSSVPLP 365

RESULT 11
AAR37215
ID AAR37215 standard; protein; 468 AA.
XX
AC AAR37215;
XX
DT 13-SEP-1993 (first entry)
XX
DE IL-6 receptor.
XX
KM Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
KM transmembrane; multiple myeloma; binding; ability; signal transfer;
KM disease; intracellular.
XX
OS Synthetic.
XX
PN JP05091892-A.
XX
PD 16-APR-1993.
XX
PR 02-OCT-1991; 91JP-00255521.
XX
PR 02-OCT-1991; 91JP-00255521.
XX
PR 02-OCT-1991; 91JP-00255521.
XX
PA (KISH/) KISHIMOTO C.
PA (CHUS) CHUGAI PHARM CO LTD.
PA (TOYJ) TOSOH CORP.
XX
DR WPI; 1993-161739/20.
XX
DR N-PSDB; AAQ41746.
XX
PT New interleukin-6 receptor deriv. - for treating diseases caused by IL-6,
PT e.g. multiple myeloma.
XX
PS Disclosure; Page 10-12; 23pp; Japanese.
XX
CC This sequence represents an interleukin-6 (IL-6) receptor. Variants of
CC the receptor lacking either the immunoglobulin-like domain or the
CC transmembrane and intracellular domain have IL-6 binding ability and
CC signal transfer ability. Either the full length or truncated IL-6
CC receptors may be used for diseases caused by IL-6 such as multiple
CC myeloma
XX
SQ Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 2; Length 468;

```

Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSTVTLTGPCVPEPDNATVHW 60
DB 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSTVTLTGPCVPEPDNATVHW 60
QY 61 VLKRPAGSHPSRMAGMRRLILRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLIS 120
DB 61 VLKRPAGSHPSRMAGMRRLILRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLIS 120
QY 121 CFRKSPLSNVVCEWGRSTPSLTITTKAVLLVRKFQNSPAEDPOPCQYQSOSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGRSTPSLTITTKAVLLVRKFQNSPAEDPOPCQYQSOSQKFSQCLAV 180
QY 181 PEDDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRSLSTWOD 240
DB 181 PEDDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRSLSTWOD 240
QY 241 PSHMNSFYRLRPELRYRABRSKFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEEFQ 300
DB 241 PSHMNSFYRLRPELRYRABRSKFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEEFQ 300
QY 301 GEMSEWSPAMGTPWTERSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360
DB 301 GEMSEWSPAMGTPWTERSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPY---- 356
QY 361 VPPGEDSKDVAAP 373
DB 357 ----QDSSSVPLP 365

RESULT 12

AAB36655
ID AAB36655 standard; protein; 468 AA.

AC AAB36655;

DT 13-MAR-2001 (first entry)

DE Human IL-6 receptor subunit alpha protein SEQ ID NO:12.

KM DNAX cytokine receptor subunit; DCRS2; receptor protein;

KW modulating cell proliferation; diagnosis; detection; drug screening;

KW immunological disorder.

OS Homo sapiens.

PN WO200073451-A1.

PD 07-DEC-2000.

PF 30-MAY-2000; 2000WO-US014867.

PR 01-JUN-1999; 99US-00322913.

PA (SCHE) SCHERING CORP.

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;

DR WPI; 2001-061536/07.

PT Novel composition comprising DNAX cytokine receptor subunit polypeptide

PS immunological disorders.

XX Disclosure; Page 13-15; 93pp; English.

CC The present invention describes a composition (I) comprising a

CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The

CC DCRS2 polypeptide is useful for binding ligands and for preparing

CC antibodies. The DCRS2 polypeptide is also useful for modulating cell

CC proliferation, for diagnostic and therapeutic applications, for detecting

CC presence of their ligands and in drug screening assays. It is also useful

CC for treating conditions such as immunological disorders. The present

CC sequence represents a cytokine receptor subunit protein which is given in

CC an alignment of various cytokine receptor subunits in the exemplification

CC of the present invention

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Query Match 67.0%; Score 1918; DB 4; Length 468;

Best Local Similarity 96.5%; Pred. No. 5e-120;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSTVTLTGPCVPEPDNATVHW 60
DB 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSTVTLTGPCVPEPDNATVHW 60
QY 61 VLKRPAGSHPSRMAGMRRLILRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLIS 120
DB 61 VLKRPAGSHPSRMAGMRRLILRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLIS 120
QY 121 CFRKSPLSNVVCEWGRSTPSLTITTKAVLLVRKFQNSPAEDPOPCQYQSOSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGRSTPSLTITTKAVLLVRKFQNSPAEDPOPCQYQSOSQKFSQCLAV 180
QY 181 PEDDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRSLSTWOD 240
DB 181 PEDDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTVAANPRSLSTWOD 240
QY 241 PSHMNSFYRLRPELRYRABRSKFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEEFQ 300
DB 241 PSHMNSFYRLRPELRYRABRSKFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEEFQ 300
QY 301 GEMSEWSPAMGTPWTERSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360
DB 301 GEMSEWSPAMGTPWTERSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPY---- 356
QY 361 VPPGEDSKDVAAP 373
DB 357 ----QDSSSVPLP 365

RESULT 13

AAE28593
ID AAE28593 standard; protein; 468 AA.

AC AAE28593;

DT 27-DEC-2002 (first entry)

DE Interleukine receptor (IL6R).

KM Hypoxia-regulated condition; tumorigenesis; angiogenesis; retinopathy;

KW inflammation; apoptosis; erythropoiesis; peripheral arterial disease;

KW cancer; ischaemia; coronary arterial disease; inflammatory condition;

KW rheumatoid arthritis; reperfusion injury; neonatal stress; infection;

KW stroke; preclampsia; atherosclerosis; cystic fibrosis; wound healing;

KW gene therapy; vaccine; interleukine receptor; IL6R.

OS Unidentified.

PN WO200268466-A2.

PD 06-SEP-2002.

PF 22-FEB-2002; 2002WO-GB000817.

PR 22-FEB-2001; 2001GB-00004440.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.

PI White J, Mundy CR, Ward NR, Krige D, Kingsman AJ, Harris RA;

XX Barber R;

DR WPI; 2002-698656/75.
DR N-PSDB; AAD45938.
XX
PT New hypoxia-regulated genes and polypeptides, useful for treating or
PT preventing hypoxia-regulated condition, e.g. tumorigenesis, angiogenesis,
PT inflammation, erythropoiesis, or the biological response to hypoxia
PT conditions.
XX
PS Claim 1; Page 106; 122pp; English.
XX
XX The invention relates to novel hypoxia-regulated polypeptides and
CC polynucleotides. Sequences of the invention are useful in therapy or
CC diagnosis of disease, particularly a hypoxia-regulated condition such as
CC tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or
CC the biological response to hypoxia conditions (including processes such
CC as glycolysis, gluconeogenesis, catecholamine synthesis, glucose
CC transport, iron transport or nitric oxide synthesis). They are also
CC useful in therapy or diagnosis of diseases or conditions affected by
CC hypoxia, e.g. cancer, ischaemic conditions (such as stroke, coronary or
CC peripheral arterial disease), reperfusion injury, neonatal stress,
CC retinopathy, preclampsia, atherosclerosis, inflammatory conditions
CC (including rheumatoid arthritis), diseases involving infections of the
CC always (such as cystic fibrosis) and wound healing. The invention is
CC useful in gene therapy and as vaccines. The present sequence is
CC interleukin6 receptor (IL6R). This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 468 AA;
Query Match 67.0%; Score 1918; DB 5; Length 468;
Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
QY 1 MLAVGCAALIAALIAAPGALAPRCPOEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
DB 1 MLAVGCAALIAALIAAPGALAPRCPOEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
QY VLRKPAAGSHPRKAGRGRLILRSVOLHDSGNYSCTRAGRPAGTVHLVDVPEEPQLS 120
DB VLRKPAAGSHPRKAGRGRLILRSVOLHDSGNYSCTRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQSFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQSFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTVAARNRMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTVAARNRMLSVTWOD 240
QY 241 PHSNNSFYRLRFELRYARSKTFTTMMVKDLOHHCVIDAMSGLRHVQQLRAQEEFGQ 300
DB 241 PHSNNSFYRLRFELRYARSKTFTTMMVKDLOHHCVIDAMSGLRHVQQLRAQEEFGQ 300
QY 301 GEMSEWSPKAGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPVEFMP 360
DB 301 GEMSEWSPKAGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPVEFMP 360
QY 361 VPPGEDSKDVAAP 373
DB 361 VPPGEDSKDVAAP 373
QY 357 ----QDSSSVLP 365
DB 357 ----QDSSSVLP 365
RESULT 14
ABB78191
ID ABB78191 standard; protein; 468 AA.
XX ABB78191;
XX
XX 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of human interleukin-6 (IL-6) receptor alpha.
DE
XX Human; interleukin-6; IL-6 receptor alpha; IL-6 alpha; IL-6; hepatocyte;

KM hepatitis B virus; HBV; glycoprotein 130; gp130; glycoprotein 80; gp80;
KM hepatitis B infection; ss.
XX
XX Homo sapiens.
XX US6410009-B1.
XX
XX 25-JUN-2002.
XX
XX 12-NOV-1999; 99US-00439856.
XX
XX 11-FEB-1997; 97US-00795473.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX Galun E, Nahor O, Blum HE;
XX
XX WPI; 2002-582017/62.
DR
XX Inhibiting or treating infection of hepatocytes by hepatitis B virus
PT using soluble agent which inhibits interaction between hIL-6 and
PT hepatocytes, particularly hyper-IL-6.
XX
XX Disclosure; Fig 9a-b; 38pp; English.
XX
XX The present sequence represents a human interleukin-6 (IL-6) receptor
CC alpha (IL-6R alpha). Fragments of IL-6 are used in the method of the
CC invention. The specification describes a method for inhibiting or
CC treating infection of hepatocytes by hepatitis B virus (HBV). The method
CC comprises administering to a human patient a soluble active agent which
CC inhibits interaction between human IL-6 and hepatocytes, and so inhibits
CC activation of glycoprotein 130 (gp130) and the internalisation of HBV
CC into the hepatocytes. The soluble agent is selected from glycoprotein 80
CC (gp80), or its portion spanning amino acids 113-323 and having receptor
CC sites that interact with IL6 and competitively inhibit interaction
CC between IL-6 and hepatocytes; glycoprotein 130 (gp130), or its portion
CC spanning amino acids 1-94 and 141-230 and having receptor sites that
CC interact with IL-6 and competitively inhibit interaction between IL-6 and
CC hepatocytes; IL-6 peptides LYS41-ALA56, GLY77-GLU95 or GLN153-HIS165;
CC and/or a combined beta1 and beta2 IL-6 mutant. The method is used to
CC prevent or treat hepatitis B infection
XX
XX Sequence 468 AA;
SQ
Query Match 67.0%; Score 1918; DB 5; Length 468;
Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
QY 1 MLAVGCAALIAALIAAPGALAPRCPOEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
DB 1 MLAVGCAALIAALIAAPGALAPRCPOEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
QY 61 VLRKPAAGSHPRKAGRGRLILRSVOLHDSGNYSCTRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLRKPAAGSHPRKAGRGRLILRSVOLHDSGNYSCTRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQSFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQSFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTVAARNRMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTVAARNRMLSVTWOD 240
QY 241 PHSNNSFYRLRFELRYARSKTFTTMMVKDLOHHCVIDAMSGLRHVQQLRAQEEFGQ 300
DB 241 PHSNNSFYRLRFELRYARSKTFTTMMVKDLOHHCVIDAMSGLRHVQQLRAQEEFGQ 300
QY 301 GEMSEWSPKAGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPVEFMP 360
DB 301 GEMSEWSPKAGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPVEFMP 360
QY 361 VPPGEDSKDVAAP 373
DB 361 VPPGEDSKDVAAP 373

Db 357 ----QDSSVPLP 365

RESULT 15

ABP72697 standard; protein; 468 AA.

ABP72697;

11-JUN-2003 (first entry)

Human interleukin-6 receptor.

Human, interleukin-6; receptor; antibacterial; virucide; anti-HIV; antirheumatic; antichratic; antiinflammatory; immunosuppressive; gene therapy.

Homo sapiens.

Homo sapiens.

Key location/Qualifiers
359..386

Domain /label= Transmembrane

WO2003014359-A2.

20-FEB-2003.

02-AUG-2002; 2002MO-GB003581.

03-AUG-2001; 2001GB-00019015.

(UYCA-) UNIV COLLEGE CARDIFF.
(UYWA-) UNIV WALES COLLEGE OF MEDICINE.

Jones SA, Topley N;

WPI; 2003-256588/25.

New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunological disorder.

Disclosure; Fig 2; 46pp; English.

The present sequence is the protein sequence of the human interleukin-6 receptor (IL-6R). A soluble receptor is obtained either through proteolytic cleavage or differential mRNA splicing of IL-6R (see ABP72698). The present invention relates to a fusion protein (see ABP72702) comprising a functional IL-6 molecule and a functional DS-sIL-6R molecule. Administration of the fusion protein results in the increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. Also claimed are a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed).

Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 6; Length 468;

Best Local Similarity 96.5%; Pred. No. 5e-120;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

1 MLAVGALLAALAAAGALAPRCAPQAVARCVTLSPDSTTLTCPCGPEPDNATVM 60

61 VLKPAAGSHPSRMAGMGRLLLRVQLHDSGNVSCYRAGRPAQVTHLVDPPEEPQLS 120

121 CRRKSPLSNVVCEMGPSPSTLTAKAVILVRFQNSPADPQPCOYSGOESKFCGLAV 180

121 CRRKSPLSNVVCEMGPSPSTLTAKAVILVRFQNSPADPQPCOYSGOESKFCGLAV 180

181 PEGDSSFYIVSMCVASVSGSKSKTQTFQCGILQPDPPANTITVAVANPMLSVTMD 240

181 PEGDSSFYIVSMCVASVSGSKSKTQTFQCGILQPDPPANTITVAVANPMLSVTMD 240

241 PHSWNSFFYRLRFEELRYAERSKFTTMMVXDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300

241 PHSWNSFFYRLRFEELRYAERSKFTTMMVXDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300

301 GEMSEWSPKAMGTPTWESRSPPAENEVSTPMQALTTNKDDNIIIPDSANATSLPYEPNP 360

301 GEMSEWSPKAMGTPTWESRSPPAENEVSTPMQALTTNKDDNIIIPDSANATSLPYEPNP 360

361 VPPGSDSKDVAAP 373

357 ----QDSSVPLP 365

RESULT 16

ADCO7187 standard; protein; 468 AA.

ADCO7187;

18-DEC-2003 (first entry)

Human IL-6 receptor subunit alpha.

Human IL-6 receptor subunit 2; DCRS2; cell physiology; cell development; cell culture; interferon detection; immune system disorder; interleukin 6; IL-6; receptor subunit alpha; human.

Homo sapiens.

US2003082734-A1.

01-MAY-2003.

18-SEP-2002; 2002US-00247463.

01-JUN-1999; 99US-0137159P.

31-MAY-2000; 2000US-00588113.

(DOWL/) DOWLING L M.

(TIMA/) TIMANS J C.

(GORM/) GORMAN D M.

(KAST/) KASTELEIN R A.

(BAZA/) BAZAN J F.

Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;

WPI; 2003-730048/69.

Composition potentially useful for treating immunological disorders, comprises a DNA cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2 sequence.

Disclosure; SEQ ID NO 12; 41pp; English.

The invention describes a composition of matter (I) comprising a substantially pure or recombinant DNA cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein comprising a DCRS2 sequence. A composition of matter comprises: a substantially pure or recombinant DCRS2 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids

CC identical to segments of a fully defined 384 amino acid sequence (S1),
 CC given in the specification; a substantially pure or recombinant DCRS2
 CC polypeptide comprising at least two distinct nonoverlapping segments of
 CC at least five amino acids identical to segments of S1; a natural sequence
 CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.
 CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating
 CC physiology or development of a cell or cell culture. Antibodies to a
 CC DCRS2 can be used for quantitative detection of interferon. The DCRS2
 CC polypeptides and nucleic acids and their binding agents are potentially
 CC useful in treating and diagnosing disease, especially disease associated
 CC with the immune system. This is the amino acid sequence of human
 CC interleukin 6 (IL-6) receptor subunit alpha used in a comparison with
 CC DCRS2.

XX Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 7; Length 468;

Best Local Similarity 96.5%; Pred. No. 5e-120;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAPAALAPRRCPAQBVARGVLTSLPQSDVTLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAPAALAPRRCPAQBVARGVLTSLPQSDVTLTCGVEPEDNATVHM 60
 QY VLKRPAGSHPSRWAGGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 DB VLKRPAGSHPSRWAGGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
 QY 181 PEGDSSFYIYVSMCVASSVGSKFTQFOCGGIIQPPPNITVTANARPRMLSTVMOD 240
 DB 181 PEGDSSFYIYVSMCVASSVGSKFTQFOCGGIIQPPPNITVTANARPRMLSTVMOD 240
 QY 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLHHVQLRAQEEFGQ 300
 DB 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLHHVQLRAQEEFGQ 300
 QY 301 GEMSEWPEAMGTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVEFMP 360
 DB 301 GEMSEWPEAMGTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVEFMP 360
 QY 361 VPPEDESKDVAP 373
 DB 357 ---QDSSSVPLP 365

RESULT 17

AA92195 ID AA92195 standard; protein; 690 AA.

XX AAY92195;

DT 01-AUG-2000 (first entry)

XX Human IL-6R-alpha-C-gamma-1 fusion protein.

XX IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
 KW fusion protein; cytosolic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..358

FT Peptide 359..360

FT Protein /note= "Ala-Gly bridge"

FT Protein 361..690

XX /label= C-gamma-4

PN MO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99MO-US022045.

XX 25-SEP-1998; 98US-0101858P.

XX 19-MAY-1999; 99US-0013942.

XX (REGG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

PT Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.

XX Example 4; Page; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor (SR-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (ciliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia

XX Sequence 690 AA;

Query Match 67.0%; Score 1917; DB 3; Length 690;

Best Local Similarity 68.9%; Pred. No. 9.4e-120;

Matches 385; Conservative 29; Mismatches 57; Indels 88; Gaps 8;

QY 1 MLAVGALLAALAAPAALAPRRCPAQBVARGVLTSLPQSDVTLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAPAALAPRRCPAQBVARGVLTSLPQSDVTLTCGVEPEDNATVHM 60
 QY VLKRPAGSHPSRWAGGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 DB VLKRPAGSHPSRWAGGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
 QY 181 PEGDSSFYIYVSMCVASSVGSKFTQFOCGGIIQPPPNITVTANARPRMLSTVMOD 240
 DB 181 PEGDSSFYIYVSMCVASSVGSKFTQFOCGGIIQPPPNITVTANARPRMLSTVMOD 240
 QY 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLHHVQLRAQEEFGQ 300
 DB 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLHHVQLRAQEEFGQ 300

QY 301 GEMSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYE--- 357
 DB 301 GEMSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYQDAG 360
 QY 358 -----FNPVPPGES-----KD-----VAAPIHROPLT----- 379
 DB 361 ASTKGPVFPPLAPSSKSTSGTAAAGCLVADYFPEPVTVSNWNGALTSQTHFPAYLQSS 420
 QY 380 -----SSERIDKQIYIIDGIALAKETCNKSNMGE 410
 DB 421 GLYSLSVVTPSSSLGDTQTYICNVNHNKPSNTKVDKVV-----EPKSCDKTHTCP 470
 QY 411 --SSKALAEANNILNPKMAEKDGFQSGFNEETCLVKIIT---GLIEFEVYLEYLQ---N 462
 DB 471 PCPABELLGSPVFLFPPKPKOTLMISRPETVTCVVVDVSHEDPEVKFMWYVDGVEVNA 530
 QY 463 RFESSEEQARAVOMSTKVL 481
 DB 531 KTKPREEQYNSTYRVSVL 549

RESULT 18

AA92196
 ID AAY92196 standard; protein; 468 AA.

AC AAY92196;
 XX

DT 01-AUG-2000 (first entry)

DE Human IL-6R-alpha-kappa fusion protein.

KM IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
 fusion protein; cytostatic; immunomodulator; osteopathic.

OS Synthetic.
 XX Homo sapiens.

Key Location/Qualifiers
 FH 1..358
 FT /label= IL-6R-alpha
 FT Peptide 359..360
 FT /note= "Ala-Gly bridge"
 FT Protein 361..468
 FT /label= kappa_domain

PN WO200018932-A2.
 XX

PD 06-APR-2000.
 XX

PF 22-SEP-1999; 99WO-US022045.
 XX

PR 25-SEP-1998; 98US-0101858P.
 PR 19-MAY-1999; 99US-00313942.
 XX

PA (REGS-) REGENERON PHARM INC.
 XX

PI Stahl N, Yancopoulos GD;
 XX

DR WPI; 2000-293165/25.
 XX

PT Isolated nucleic acid molecule for treating cytokine-related diseases or
 disorders encodes a fusion polypeptide capable of binding a cytokine to
 form a nonfunctional complex.
 PT

XX Example 4; Page; 152pp; English.
 XX

CC The invention concerns production of antagonists to any cytokine that
 utilizes an alpha specificity determining component, which when combined
 with the cytokine, binds to a first beta signal transducing component to
 form a non-functional intermediate which then binds to a second beta
 signal transducing component causing beta-receptor dimerization, the
 soluble alpha specificity determining component of the receptor (8R-
 alpha) and the extracellular domain of the first beta signal transducing

CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (8R-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (cellary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia
 XX

Sequence 468 AA;

Query Match 67.0%; Score 1915.5; DB 3; Length 468;

Best Local Similarity 83.8%; Pred. No. 7.3e-120; Mismatches 28; Indels 33; Gaps 5;

Matches 373; Conservative 11; Mismatches 28; Indels 33; Gaps 5;

QY 1 MLAVGCAALAAALAAAGALAPRCPCPAQEVAGVLTSLPGDSVTLCPGVEPEDNATVHM 60

DB 1 MYAVGCAALAAALAAAGALAPRCPCPAQEVAGVLTSLPGDSVTLCPGVEPEDNATVHM 60

QY 61 VLRKPAAGSHPRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPEEPQLS 120

DB 61 VLRKPAAGSHPRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPEEPQLS 120

QY 121 CRRKSPLSNVCEMGRSTPSLTTXAVLLVRFQNSPADPQPCQYSGESQKFCQLAV 180

DB 121 CRRKSPLSNVCEMGRSTPSLTTXAVLLVRFQNSPADPQPCQYSGESQKFCQLAV 180

QY 181 PGDSSFYIVSMCVASVSGSKFTQTFQGCGLQDPDPANITVTVAANPWLSTWQD 240

DB 181 PGDSSFYIVSMCVASVSGSKFTQTFQGCGLQDPDPANITVTVAANPWLSTWQD 240

QY 241 PHSWNSFYRLRPELRRAERSKFTTMMVKLOHHCVTHDMSGIRHVVQLRAGEEFCQ 300

DB 241 PHSWNSFYRLRPELRRAERSKFTTMMVKLOHHCVTHDMSGIRHVVQLRAGEEFCQ 300

QY 301 GEMSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFP 360

DB 301 GEMSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPYEFP 360

QY 361 VPPGEDSKVAAPIHQPLTSSERIDKQIYIIDGIALAKETCNKSNMCESSKEALAEEN 420

DB 361 VPPGEDSKVAAPIHQPLTSSERIDKQIYIIDGIALAKETCNKSNMCESSKEALAEEN 420

QY 421 LNLIPKMA---EKDGFQSGFNEET 441

DB 421 LNLIPKMA---EKDGFQSGFNEET 441

QY 394 --YPREAKYQWKVDNALQSGNSQES 416

DB 394 --YPREAKYQWKVDNALQSGNSQES 416

QY 421 LNLIPKMA---EKDGFQSGFNEET 441

DB 421 LNLIPKMA---EKDGFQSGFNEET 441

QY 28-NOV-1996 (first entry)

DB 28-NOV-1996 (first entry)

QY Interleukin-6 receptor.
 XX Interleukin-6; IL; receptor; antinease oligonucleotide; inhibition;
 KW gene expression; kidney tumor; myeloma; Kaposi's sarcoma; psoriasis;
 KW rheumatoid arthritis; endotoxic shock.
 XX Homo sapiens.

XX MO9618416-A1.
 XX 20-JUN-1996.
 XX 15-DEC-1995; 95MO-JF002587.
 XX 16-DEC-1994; 94JD-00313167.
 PR 18-AUG-1995; 95JD-00210739.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Kuromaru K, Koishibara Y;
 XX WPI; 1996-300392/30.
 DR N-PSDB; NAT31441.
 XX Anti-sense oligo:nucleotide inhibitor against human IL-6R expression -
 PT for treatment of e.g. tumours, cancers, rheumatoid arthritis, psoriasis,
 PT endo:toxic shock, etc.
 XX Claim 2; Page 17-21; 32pp; Japanese.
 XX Antisense oligonucleotides may be used to inhibit the expression of the
 CC interleukin-6 receptor. Inhibition of expression of the IL-6 receptor is
 CC useful in the treatment of kidney tumours, myeloma, Kaposi's sarcoma,
 CC rheumatoid arthritis, psoriasis and endotoxic shock. The antisense
 CC oligonucleotides are administered at a dosage of 0.1-100mg/kg, pref. 0.1-
 CC 50 mg/kg
 XX Sequence 468 AA;
 XX SQ
 Query Match 66.9%; Score 1915; DB 2; Length 468;
 Best Local Similarity 96.2%; Pred. No. 7.9e-120;
 Matches 359; Conservative 2; Mismatches 4; Indels 8; Gaps 1;
 QY 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDPPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDPPEEPQLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVQVLAQEEFQ 300
 DB 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVQVLAQEEFQ 300
 QY 301 GEMSEWSPKMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRDSANATSLPVEFW 360
 DB 301 GEMSEWSPKMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRDSANATSLPVEFW 360
 QY 361 VPPGEDSKVAAAP 373
 DB 357 ----QDSSSVPLP 365

RESULT 20
 ABP72699
 ID ABP72699 standard; protein; 357 AA.
 XX ABP72699;
 XX AC
 XX DT 11-JUN-2003 (first entry)
 XX

DE Soluble interleukin-6 receptor isoform PC-sIL-6R.
 XX Human; interleukin-6; receptor; PC-sIL-6R; antibacterial; virucide;
 KW anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
 KW immunosuppressive; gene therapy.
 XX Homo sapiens.
 XX WO2003014359-A2.
 XX 20-FEB-2003.
 XX 02-AUG-2002; 2002WO-GB003581.
 XX 03-AUG-2001; 2001GB-00019015.
 XX (UYWA-) UNIV COLLEGE CARDIFF.
 XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX Jones SA, Topley N;
 XX WPI; 2003-256588/25.
 XX The present sequence is the protein sequence of a soluble form of the
 CC human interleukin-6 receptor (IL-6R), denoted PC-sIL-6R, produced by
 CC proteolytic cleavage. A fusion protein of human IL-6 and PC-sIL-6R
 CC increases expression of MCP-1, but unlike a novel fusion protein of the
 CC invention (see ABP72702) comprising IL-6 and DS-sIL-6R, does not increase
 CC expression of MIP-1alpha, MIP-1beta, RANTES or IP-10. The invention
 CC relates to this novel fusion protein and its use in the prophylaxis or
 CC treatment of an infectious disease (especially AIDS caused by a M-tropic
 CC strain of HIV, or bacterial peritonitis), an inflammatory disorder or an
 CC immunological disorder (especially rheumatoid arthritis), when it is
 CC desirable to increase or resolve an immune response
 XX SQ
 Query Match 66.9%; Score 1913; DB 6; Length 357;
 Best Local Similarity 99.7%; Pred. No. 7.7e-120;
 Matches 356; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDPPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDPPEEPQLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVLVKRFQNSPAEDFOECYQSOESQKFSQCLAV 180
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVQVLAQEEFQ 300
 DB 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVQVLAQEEFQ 300
 QY 301 GEMSEWSPKMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRDSANATSLPVEFW 357
 DB 301 GEMSEWSPKMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRDSANATSLPVEFW 357

RESULT 21
 ID AAY92197 standard; protein, 477 AA:
 AAY92197
 AC AAY92197;
 DT 01-AUG-2000 (first entry)
 DE Human IL-6R-alpha-j-kappa fusion protein.
 KM IL-6R-alpha-j-kappa; cytokine; antagonist; CNTF; receptor;
 KM fusion protein; cytosolic; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN MO200018932-A2.
 PD 06-APR-2000.
 PF 22-SEP-1999; 99WO-US022045.
 PR 25-SEP-1998; 98US-010185AP.
 PR 19-MAY-1999; 99US-00313942.
 PA (REGG-) REGENERON PHARM INC.
 PI Stahl N, Yancopoulos GD;
 DR WPI, 2000-293165/25.
 XX
 XX Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PR form a nonfunctional complex.
 PS
 PS Example 4; Page; 152pp; English.
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specifically determining component of the receptor (SR-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (gliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specifically determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia
 QQ Sequence 477 AA:

QY	61	YLRKPAAGSHPRMAGMRGRLLRLSVOLHDSGNTSVCRAGRPAGTVALHLDVPEEPQLS	120
Db	61	YLRKPAAGSHPRMAGMRGRLLRLSVOLHDSGNTSVCRAGRPAGTVALHLDVPEEPQLS	120
QY	121	CFKPSBLNVVCEWGPSTPSLTTKAVLLVRFQNSPAEDFQOEBCOYSQESQKFSQCLAV	180
Db	121	CFKPSBLNVVCEWGPSTPSLTTKAVLLVRFQNSPAEDFQOEBCOYSQESQKFSQCLAV	180
QY	181	PBEDSFFIYVSNCAVSSVGSKFSTQTQGGGIIQPPRANITTTAVARPRMLSTWOD	240
Db	181	PBEDSFFIYVSNCAVSSVGSKFSTQTQGGGIIQPPRANITTTAVARPRMLSTWOD	240
QY	241	PHSMNSFFRLRFBRLRYRABRSKPTTMMVMDLOHCHYHDAWGLRHVVQLRAQEEFGQ	300
Db	241	PHSMNSFFRLRFBRLRYRABRSKPTTMMVMDLOHCHYHDAWGLRHVVQLRAQEEFGQ	300
QY	301	GEWSEWSPAMGCTPWTESRSPAPAEVNSTPMQALTTNKDDNILLFRDSANATSLPVE---	357
Db	301	GEWSEWSPAMGCTPWTESRSPAPAEVNSTPMQALTTNKDDNILLFRDSANATSLPVDAG	360
QY	358	-FMVPPPGF---DSKDVAAPIHQPLTSSERIKDQIRYILDGIALRKETCNKSNMCESS	412
Db	361	TF-----GGGTVEIKETVAAPSVFIFPPS---DEOLK-----SGTASVCLLNPF----	402
QY	413	KEALAEENNLPLPKMA-----EKDQCGSGSPNEET	441
Db	403	-----YFREAKVQMKVDNALQSNLSQDS	425

Accession	Protein Name	Length (aa)	Source	Keywords	Notes
AAW70804	standard; protein; 360 AA.	360	Human	cytokine; interleukin-6	
AAW70804					
03-FEB-1999	(first entry)				
DE	Amino acid sequence of the interleukin (IL)-6R-alpha domain.				
XX					
XX	gp130; cytokine antagonist; interleukin; gamma-interferon;				
KM	granulocyte macrophage colony-stimulating factor; J peptide;				
XX	transforming growth factor-beta.				
OS	Synthetic.				
XX					
Key	Location/Qualifiers				
FT	1..358				
FT	Protein				
FT	/note="soluble interleukin (IL)-6R-alpha domain"				
XX					
FN	US5844099-A.				
XX					
PD	01-DEC-1998.				
XX					
PF	27-NOV-1995; 95US-00563105.				
XX					
PR	20-OCT-1993; 93US-00140222.				
XX					
PA	(REGG-) REGENERON PHARM INC.				
XX					
PI	Yancopoulos GD, Stahl N, Economides A;				
XX					
DR	WPI; 1999-044669/04.				
XX					
PT	Cytokine antagonists - comprising extracellular domains of specificity-				
XX	determining and signal-transducing components of cytokine receptor.				
FT					
XX					
PS	Example 4; Fig 15; 46p; English.				
XX					
CC	The present sequence represents the amino acid sequence of interleukin				
CC	(IL)-6R-alpha domain. The protein is used in the course of the invention.				
CC	The specification describes cytokine antagonists comprising only the				
CC	extracellular domain of the specificity-determining component of the				
CC	cytokine receptor and the extracellular domain of a signal-transducing				

CC component of the cytokine receptor. The cytokine is an interleukin (IL-1,
 CC IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte macrophage colony-
 CC stimulating factor (GM-CSF), gamma-interferon or transforming growth
 CC factor-beta (TGF-beta). The antagonist is capable of binding the cytokine
 CC to form a nonfunctional complex. The compound has therapeutic activity
 CC as cytokine antagonists and can also be used in assays for identifying
 CC novel agonists and antagonists of cytokines

XX Sequence 360 AA;

Query Match 66.8%; Score 1910; DB 2; Length 360;

Best Local Similarity 99.4%; Pred. No. 1,2e-119; Indels 0; Gaps 0;

Matches 355; Conservative 2; Mismatches 0;

QY 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPDSDVTLTCGVEPEDNATVHM 60
 Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPDSDVTLTCGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGPSTSLTTKAVLLVRKQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFFKSPLSNVVCEWGPSTSLTTKAVLLVRKQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 QY 241 PHSWNSFYRLRPFLRYRARSKTFTTMMVKDLOHHCVILDHWSGLRHVVQLRAQEEFQ 300
 Db 241 PHSWNSFYRLRPFLRYRARSKTFTTMMVKDLOHHCVILDHWSGLRHVVQLRAQEEFQ 300
 QY 301 GEWSWSPBAMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRSANATSLPVE 357
 Db 301 GEWSWSPBAMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRSANATSLPVE 357

RESULT 23

AAV92199 standard; protein; 360 AA.

XX AAV92199;

DT 01-AUG-2000 (first entry)

XX Soluble human IL-6-R-alpha.

XX Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor;

KW fusion protein; cytosolic; immunomodulator; osteopathic.

XX Homo sapiens.

PN WO200018932-A2.

PD 06-APR-2000.

PF 22-SEP-1999; 99WO-US022045.

PR 25-SEP-1998; 98US-0101858P.

PR 19-MAY-1999; 99US-00313942.

PA (REG-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

DR WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.

PS Example 4; Fig 15; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor (SR-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (ciliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia

XX Sequence 360 AA;

Query Match 66.8%; Score 1910; DB 3; Length 360;

Best Local Similarity 99.4%; Pred. No. 1,2e-119; Indels 0; Gaps 0;

Matches 355; Conservative 2; Mismatches 0;

QY 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPDSDVTLTCGVEPEDNATVHM 60
 Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPDSDVTLTCGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGPSTSLTTKAVLLVRKQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFFKSPLSNVVCEWGPSTSLTTKAVLLVRKQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 QY 241 PHSWNSFYRLRPFLRYRARSKTFTTMMVKDLOHHCVILDHWSGLRHVVQLRAQEEFQ 300
 Db 241 PHSWNSFYRLRPFLRYRARSKTFTTMMVKDLOHHCVILDHWSGLRHVVQLRAQEEFQ 300
 QY 301 GEWSWSPBAMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRSANATSLPVE 357
 Db 301 GEWSWSPBAMGTPWTESRSPPAENESTPMQALTTNKDDNILLFRSANATSLPVE 357

RESULT 24

ABW02172 standard; protein; 360 AA.

XX ABW02172;

AC 12-FEB-2004 (first entry)

DE Human IL-6Ralpha-domain protein.

XX Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
 KW cancer; cachexia; arthritis; cytosolic; osteopathic; therapy; human.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..358 "Human IL-6alpha-domain"
 FT /note="Human IL-6alpha-domain"
 FT Region 99..100
 FT /note="Ala-Gly bridge"
 XX US2003143697-A1.
 XX 31-JUL-2003.
 XX 28-OCT-2002; 2002US-00282162.
 XX 22-SEP-1999; 99WO-US022045.
 PR 22-MAR-2001; 2001US-00787835.
 XX (STAH/) STAHL N.
 PA (YANC/) YANCOPOULOS G D.
 XX Stahl N, Yancopoulos GD;
 PI WPI, 2003-851784/79.
 DR New nucleic acid molecules encoding fusion polypeptides capable of
 XX binding a cytokine to form a non-functional complex, useful for treating
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 PT or osteoporosis.
 XX Example 4; Fig 15; 300pp; English.
 XX The present invention provides a novel fusion polypeptide capable of
 CC binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human IL-
 CC 6alpha-domain protein
 XX
 XX Sequence 360 AA;
 SQ
 Query Match 66.8%; Score 1910; DB 7; Length 360;
 Best Local Similarity 99.4%; Pred. No. 1.2e-119;
 Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 DB 1 MAAVGCALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 QY 121 CPERKSPLSNVVCEWGRSTPSLTAKVLLVRKFQNSPADFOEPCQYSGSQKFSQCLAV 180
 DB 121 CPERKSPLSNVVCEWGRSTPSLTAKVLLVRKFQNSPADFOEPCQYSGSQKFSQCLAV 180
 QY 181 PEDSSFFIYVSMCVASVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 DB 181 PEDSSFFIYVSMCVASVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 QY 241 PHSWNSFFRLRFELRYRARSKTFTTMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 DB 241 PHSWNSFFRLRFELRYRARSKTFTTMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 357
 DB 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 357
 RESULT 25
 AAP90525 standard; protein; 468 AA.
 XX
 AC AAP90525;

XX 25-MAR-2003 (revised)
 DT 23-JAN-1990 (first entry)
 XX B cell stimulating factor-2 receptor.
 DE B cell stimulating factor-2 receptor.
 XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 XX AU8928720-A.
 XX 27-JUL-1989.
 XX 23-JAN-1989; 89AU-00028720.
 PR 14-JAN-1989; 89JP-00007461.
 XX (KISH/) KISHIMOTO T.
 PA
 XX WPI; 1989-264012/37.
 DR N-PSDB; AAP90525.
 XX Receptor protein for human B cell stimulatory factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for associated
 PT disorders.
 XX Claim 2; Page 36; 76pp; English.
 XX The BSF2 receptor is derived from a monocytic U937 cell line. It can be
 CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
 CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
 CC used to study an immune mechanism with which BSF-2 or the receptor is
 CC concerned. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 468 AA;
 SQ
 Query Match 66.8%; Score 1910; DB 1; Length 468;
 Best Local Similarity 96.2%; Pred. No. 1.7e-119;
 Matches 359; Conservative 1; Mismatches 5; Indels 8; Gaps 1;
 QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 DB 1 MAAVGCALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 QY 121 CPERKSPLSNVVCEWGRSTPSLTAKVLLVRKFQNSPADFOEPCQYSGSQKFSQCLAV 180
 DB 121 CPERKSPLSNVVCEWGRSTPSLTAKVLLVRKFQNSPADFOEPCQYSGSQKFSQCLAV 180
 QY 181 PEDSSFFIYVSMCVASVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 DB 181 PEDSSFFIYVSMCVASVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 QY 241 PHSWNSFFRLRFELRYRARSKTFTTMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 DB 241 PHSWNSFFRLRFELRYRARSKTFTTMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 360
 DB 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 360
 QY 361 VPPEGDSKDVAA 373
 DB 357 ----QDSSSVLP 365
 RESULT 26
 ABP72698 standard; protein; 364 AA.
 ID ABP72698

XX ABP72698;
AC
XX
DT 11-JUN-2003 (first entry)
DE Soluble interleukin-6 receptor isoform DS-sil-6R.
XX
XX Human; interleukin-6; receptor; DS-sil-6R; antibacterial; virucide;
KM anti-HIV; antipneumatic; antiarthritic; antiinflammatory;
KM immunosuppressive; gene therapy.
XX
OS Homo sapiens.
XX
XX WQ003014359-A2.
XX
XX 20-FEB-2003.
XX
XX 02-AUG-2002; 2002MO-GB003581.
XX
XX 03-AUG-2001; 2001GB-00019015.
XX
XX (UYCA-) UNIV COLLEGE CARDIFF.
XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
XX
XX Jones SA, Topley N;
XX
XX WPI; 2003-256588/25.
XX
XX
XX New fusion protein having a functional IL-6 and DS-sil-6R molecule,
PT useful for the manufacture of a medicament for the prophylaxis or
PT treatment of an infectious disease, and an inflammatory or immunological
PT disorder.
XX
XX
XX Disclosure; Fig 4; 46pp; English.
XX
XX The present sequence is the protein sequence of a soluble form of the
CC human interleukin-6 receptor (IL-6R), denoted DS-sil-6R, produced by
CC differential mRNA splicing. The invention relates to a fusion protein
CC (see ABP72702) comprising a functional IL-6 molecule and a functional DS-
CC sil-6R molecule. Administration of the fusion protein results in the
CC increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or
CC IP-10. High levels of MIP-1alpha, MIP-1beta and RANTES complete with HIV
CC for binding to CCR5 and effectively suppress HIV entry. The fusion
CC protein can be used in the treatment of any disease in which the
CC infectious agent binds to CCR5, especially M-trophic strains of HIV. The
CC invention also provides a nucleic acid molecule encoding the fusion
CC protein, an expression vector, a host cell, and a method of producing the
CC fusion protein in the host cell. The fusion protein, nucleic acid or
CC vector can be used in the manufacture of a medicament for the prophylaxis
CC or treatment of an infectious disease (especially AIDS caused by a M-
CC tropic strain of HIV, or bacterial peritonitis), an inflammatory
CC disorder or an immunological disorder (especially rheumatoid arthritis),
CC when it is desirable to increase or resolve an immune response (claimed)
XX
XX
XX Sequence 364 AA;
SQ
Query Match 66.7%; Score 1907; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 2e-119;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVTAVARNRMLSVTWOD 240
QY 241 PHSNNSFYRLRRLRYEARSKTFTTMVVKLOCHHCVHDMSGRLHVYQVRAQREFPQ 300
DB 241 PHSNNSFYRLRRLRYEARSKTFTTMVVKLOCHHCVHDMSGRLHVYQVRAQREFPQ 300
QY 301 GEWSSESPAMGCPMTESRSPAEENEVSTPMQALTNKDDNITLFRDSANATSLP 355
DB 301 GEWSSESPAMGCPMTESRSPAEENEVSTPMQALTNKDDNITLFRDSANATSLP 355

RESULT 27
AAW71371
ID AAW71371 standard; protein; 468 AA.
XX
XX
XX AAW71371;
AC
XX
XX 02-FEB-1999 (first entry)
XX
XX
XX Human interleukin-6 receptor alpha polypeptide.
XX
XX Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
XX therapy.
XX
XX Homo sapiens.
XX
XX WQ9835694-A2.
XX
XX 20-AUG-1998.
XX
XX 10-FEB-1998; 98MO-US008898.
XX
XX 11-FEB-1997; 97US-00795473.
XX
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (DAVI-) DAVIDSON C M.
XX
XX WPI; 1998-520755/44.
XX

PT Treatment of hepatitis B virus infection - using a soluble active agent
PT which prevents interaction of HBV with hepatocytes mediated by human
PT interleukin 6.
XX
XX
XX Disclosure; Fig 9; 51pp; English.
XX
XX

CC This is a previously reported amino acid sequence for human interleukin-6
CC (hIL-6) receptor alpha. The invention relates to the finding that hIL-6
CC is essential for hepatitis B virus (HBV) infection. The invention
CC provides a pharmaceutical composition for the treatment of HBV infection,
CC comprising a soluble active agent that interacts with at least one of the
CC binding sites between hIL-6 and the psi region of HBV and between hIL-6
CC and hepatocytes and other HBV-permissive cells. The active agent
CC competitively binds to at least one of these sites and thereby prevents
CC hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive
CC cells. The soluble active agent is selected from glycoprotein 80 (gp80)
CC having receptor sites which interact with hIL-6, soluble glycoprotein 130
CC (gp130) having receptor sites which interact with hIL-6, hIL-6 derived
CC peptide Lys41-1456, hIL-6 derived peptide Gly77-Glu95, hIL-6 derived
CC peptide Glu153-His165, a combined 1 and 2 hIL-6 mutant (mhIL-6 1+2), and
CC mhIL-6 1+2 substituted with Phe171 to Leu and Ser177 to Arg, and mixtures
CC of any of these
XX
XX

SQ Sequence 468 AA;
SQ

Query Match 66.4%; Score 1900; DB 2; Length 468;
Best Local Similarity 95.4%; Pred. No. 8e-119;
Matches 356; Conservative 5; Mismatches 4; Indels 8; Gaps 1;

QY 1 MIAVGCALALALAAFGAALAPRCRPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
DB 1 MIAVGCALALALAAFGAALAPRCRPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

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QY 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
DB 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
QY 121 CERKSPLSNVCEWCEWGRSTPSTLTAKVLLVRKFQNSPADDFQPCQYSOESQKFSQCLAV 180
DB 121 CERKSPLSNVCEWCEWGRSTPSTLTAKVLLVRKFQNSPADDFQPCQYSOESQKFSQCLAV 180
QY 181 PEGDSSFFYIVSMCVASVSGSKFTQTFQCGGILQDPDPANITVTVAANPRMLSVTWOD 240
DB 181 PEGDSSFFYIVSMCVASVSGSKFTQTFQCGGILQDPDPANITVTVAANPRMLSVTWOD 240
QY 241 PHSWNSFFYRLRPELRYRERSTFTTMMVKDLOHHCVIHDAWGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFFYRLRPELRYRERSTFTTMMVKDLOHHCVIHDAWGLRHVVQLRAQEFQ 300
QY 301 GESEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNITLFPDSANATSLPYEFMP 360
DB 301 GESEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNITLFPDSANATSLPYEFMP 360
QY 361 VPPGESSKDVAAAP 373
DB 361 VPPGESSKDVAAAP 373
QY 357 ---QDSSSVPLP 365
DB 357 ---QDSSSVPLP 365

```

RESULT 28

AAV55071
ID AAV55071 standard; protein; 345 AA.

AAV55071;

25-FEB-2000 (first entry)

SR345 protein sequence.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secreted functional protein; antigenic protein;
KM protein isolation; diagnosis; SR345 protein.

OS Homo sapiens.

PN WO9960113-A1.

25-NOV-1999.

30-APR-1999; 99WO-UP002341.

20-MAY-1998; 98JP-00138652.

01-OCT-1998; 98JP-00279876.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Saito M, Ohtomo T;

WPI; 2000-039382/03.

N-PSDB; AA240288.

PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

PS Example 1; Page 48-52; 120pp; Japanese.

XX This sequence represents the SR345 protein. The invention relates to a
CC method for isolating a gene encoding a membrane-bound protein, comprising
CC introducing a vector into a cell, contacting an antigen with the cell
CC expressing the fused protein encoded by the vector on its surface to
CC select an antigen-binding cell, and isolating the cDNA. The vector
CC contains DNA encoding a secreted functional protein with antigenicity
CC and binding affinity, and a cDNA ligated to DNA downstream of the 3' end
CC of the coding sequence. The method can be used to isolate a membrane-
CC bound protein for diagnosis and study. It can also be used for producing
CC drugs treating abnormal functions of the protein. Such a technique is

CC efficient and selective, which is different from the prior-art
CC transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

XX Sequence 345 AA;

Query Match 64.9%; Score 1858; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.6e-116;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MIAVGCALLAAILAALPAGALAPRCPAQEVARGVLTSLPQDSVTLTCPGVEPBDNATVHM 60
DB 1 MIAVGCALLAAILAALPAGALAPRCPAQEVARGVLTSLPQDSVTLTCPGVEPBDNATVHM 60
QY 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
DB 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
QY 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
DB 61 VLKPKAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLIS 120
QY 121 CERKSPLSNVCEWCEWGRSTPSTLTAKVLLVRKFQNSPADDFQPCQYSOESQKFSQCLAV 180
DB 121 CERKSPLSNVCEWCEWGRSTPSTLTAKVLLVRKFQNSPADDFQPCQYSOESQKFSQCLAV 180
QY 181 PEGDSSFFYIVSMCVASVSGSKFTQTFQCGGILQDPDPANITVTVAANPRMLSVTWOD 240
DB 181 PEGDSSFFYIVSMCVASVSGSKFTQTFQCGGILQDPDPANITVTVAANPRMLSVTWOD 240
QY 241 PHSWNSFFYRLRPELRYRERSTFTTMMVKDLOHHCVIHDAWGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFFYRLRPELRYRERSTFTTMMVKDLOHHCVIHDAWGLRHVVQLRAQEFQ 300
QY 301 GESEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNITLFPDSANATSLPYEFMP 345
DB 301 GESEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNITLFPDSANATSLPYEFMP 345

```

RESULT 29

AAV90528
ID AAV90528 standard; protein; 344 AA.

AAV90528;

25-MAR-2003 (revised)

25-JAN-1990 (first entry)

B cell stimulating factor-2 receptor.

XX B cell stimulating factor-2 receptor; monocytic U937 cell line.

OS Homo sapiens.

PN AU8928720-A.

27-JUL-1989.

23-JAN-1989; 89AU-00028720.

14-JAN-1989; 89JP-00007461.

(KISH/) KISHIMOTO T.

WPI; 1989-264012/37.

N-PSDB; AAV90525.

PT Receptor protein for human B cell stimulatory factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for associated
PT disorders.

PS Claim 7; Page 40; 76pp; English.

XX The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to

CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 344 AA;

Query Match 64.7%; Score 1852; DB 1; Length 344;
 Best Local Similarity 100.0%; Pred. No. 9e-116;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAAGCALIAALAAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 DB 1 MVAAGCALIAALAAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMRRLLRVSQVLDHSGNVCYRAGRPAQVTHLLVDVPEEPOLS 120
 DB 61 VLKPPAAGSHPSRWAGMRRLLRVSQVLDHSGNVCYRAGRPAQVTHLLVDVPEEPOLS 120
 QY 121 CFRKSPISNVVCEWGPSTPSLTTKAVLLVRKQNSPAEDFOEPCQYSQESQFSCQAV 180
 DB 121 CFRKSPISNVVCEWGPSTPSLTTKAVLLVRKQNSPAEDFOEPCQYSQESQFSCQAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRLSVTWD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRLSVTWD 240
 QY 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
 DB 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
 QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLL 344
 DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLL 344

RESULT 30
 AAY92205
 ID AAY92205 standard; protein; 1158 AA.

XX AAY92205;

DT 01-AUG-2000 (first entry)

XX Fusion polypeptide 616, IL-6 trap.

DE IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein;

KW cytosolic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX WO200018932-A2.

PN 06-APR-2000.

XX 22-SEP-1999; 99WO-US022045.

XX 25-SEP-1998; 98US-0101858P.

PR 19-MAY-1999; 99US-00313942.

XX (REGG-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

XX WPI, 2000-293165/25.

DR N-PSDB; AAA09047.

XX Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.

XX Example 6; Fig 25A-F; 152pp; English.

XX This sequence shows fusion polypeptide 616, which is capable of binding

CC cytokine IL-6 to form a non-functional complex. The invention concerns
 CC production of antagonists to any cytokine that utilizes an alpha
 CC specificity determining component, which when combined with the cytokine,
 CC binds to a first beta signal transducing component to form a non-
 CC functional intermediate which then binds to a second beta signal
 CC transducing component causing beta-receptor dimerization, the soluble
 CC alpha specificity determining component of the receptor (SR-alpha) and
 CC the extracellular domain of the first beta signal transducing component
 CC of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
 CC alpha:beta-1) that act as antagonist to the cytokine by binding the
 CC cytokine to form a non-functional complex. The receptor components are
 CC shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
 CC of cytokines. The invention provides the basis for the development of IL-
 CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
 CC functional intermediate complex, consisting of the ligand, its alpha
 CC receptor and its beta-1 receptor component, can be formed, it will
 CC effectively block the action of the ligand. Effective antagonists of IL-6
 CC or CNTF consist of heterodimers of the extracellular domains of the alpha
 CC specificity determining components of their receptors and the
 CC extracellular domain of gp130. The resultant heterodimers, function as
 CC high-affinity traps, rendering the cytokine inaccessible to form a signal
 CC transducing complex with the native membrane-bound forms of their
 CC receptor. The nucleic acids and polypeptides are useful for treating
 CC cytokine-related diseases or disorders such as osteoporosis and primary
 CC and secondary effects of cancer including multiple myeloma or cachexia

XX Sequence 1158 AA;

Query Match 62.5%; Score 1788; DB 3; Length 1158;
 Best Local Similarity 99.1%; Pred. No. 7.8e-111;
 Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAAGCALIAALAAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 DB 1 MVAAGCALIAALAAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMRRLLRVSQVLDHSGNVCYRAGRPAQVTHLLVDVPEEPOLS 120
 DB 61 VLKPPAAGSHPSRWAGMRRLLRVSQVLDHSGNVCYRAGRPAQVTHLLVDVPEEPOLS 120
 QY 121 CFRKSPISNVVCEWGPSTPSLTTKAVLLVRKQNSPAEDFOEPCQYSQESQFSCQAV 180
 DB 121 CFRKSPISNVVCEWGPSTPSLTTKAVLLVRKQNSPAEDFOEPCQYSQESQFSCQAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRLSVTWD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRLSVTWD 240
 QY 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
 DB 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
 QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQAL 334
 DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQAL 334

RESULT 31
 ABM02178
 ID ABM02178 standard; protein; 1158 AA.

XX ABM02178;

DT 12-FEB-2004 (first entry)

XX Human cytokine trap-616 protein.

XX Cytokine; cytokine-related disease; immunomodulator; osteoporosis;

KW cancer; cachexia; arthritis; cytosolic; osteopathic; therapy; human.

XX Homo sapiens.

XX US2003143697-A1.

PN

XX 31-JUL-2003.
 PD Best Local Similarity 99.1%; Score 1788; DB 7; Length 1158;
 XX 28-OCT-2002; 2002US-00282162.
 XX
 XX 22-SEP-1999; 99WO-US022045.
 XX PR 22-MAR-2001; 2001US-00787835.
 XX
 XX (STAH/) STAHL N.
 XX (YANC/) YANCOPULOS G D.
 XX Stahl N, Yancopoulos GD;
 XX
 XX MPI: 2003-851784/79.
 XX N-PSDB; AAD63741.
 DR
 XX New nucleic acid molecules encoding fusion polypeptides capable of
 PT binding a cytokine to form a non-functional complex, useful for treating
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 PT or osteoporosis.
 XX
 XX Disclosure; Fig 25; 300pp; English.
 XX
 XX The present invention provides a novel fusion polypeptide capable of
 CC binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human
 CC cytokine trap protein
 CC
 CC Sequence 1158 AA;
 SQ

Query Match 62.5%; Score 1788; DB 7; Length 1158;
 Best Local Similarity 99.1%; Pred. No. 7.8e-110; Indels 0; Gaps 0;
 Matches 331; Conservative 2; Mismatches 1;
 QY 1 MLAVGCAALAAALAAAGALAPRCPAQEVAVGVLTSLPGDSVTLTLCPGVEPEDNATVHM 60
 DB 1 MVAVGCAALAAALAAAGALAPRCPAQEVAVGVLTSLPGDSVTLTLCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLLRSLVQLHDSGNYSCYRAGRPAAGTVHLLVDVPEBPOL 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLLRSLVQLHDSGNYSCYRAGRPAAGTVHLLVDVPEBPOL 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPFCQYSDSOKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPFCQYSDSOKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAAKPRALSTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAAKPRALSTWOD 240
 QY 241 PHSWNSFYRLRELRRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLAQQEFG 300
 DB 241 PHSWNSFYRLRELRRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLAQQEFG 300
 QY 301 GEMSEWSPAMGTPWTESRSPPAENEVSPTMQL 334
 DB 301 GEMSEWSPAMGTPWTESRSPPAENEVSPTMQL 334

RESULT 32
 ID AAY92204 standard; proteoin; 1168 AA.
 XX AAY92204;
 AC AAY92204;
 XX
 XX 01-ANG-2000 (first entry)
 DT
 XX Fusion polypeptide 412, IL-6 trap.
 DE
 XX IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
 KW cytostatic; immunomodulator; osteopathic.

XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO200018932-A2.
 XX
 XX 06-APR-2000.
 XX
 XX 22-SEP-1999; 99WO-US022045.
 XX
 XX 25-SEP-1998; 98US-0101858P.
 XX PR 19-MAY-1999; 99US-00313942.
 XX
 XX (REGG-) REGENERON PHARM INC.
 XX
 XX Stahl N, Yancopoulos GD;
 PI
 XX MPI: 2000-293165/25.
 XX N-PSDB; AAA09046.
 DR
 XX Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.
 XX
 XX Example 6; Fig 24A-F; 152pp; English.

This sequence shows fusion polypeptide 412, which is capable of binding
 CC cytokine IL-6 to form a non-functional complex. The invention concerns
 CC production of antagonists to any cytokine that utilizes an alpha
 CC specificity determining component, which when combined with the cytokine,
 CC binds to a first beta signal transducing component to form a non-
 CC functional intermediate which then binds to a second beta signal
 CC transducing component causing beta-receptor dimerization, the soluble
 CC alpha specificity determining component of the receptor (SR-alpha) and
 CC the extracellular domain of the first beta signal transducing component
 CC of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
 CC alpha:beta-1) that act as antagonist to the cytokine by binding the
 CC cytokien to form a non-functional complex. The receptor components are
 CC shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
 CC of cytokines. The invention provides the basis for the development of IL-
 CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
 CC functional intermediate complex, consisting of the ligand, its alpha
 CC receptor and its beta-1 receptor component, can be formed, it will
 CC effectively block the action of the ligand. Effective antagonists of IL-6
 CC or CNTF consist of heterodimers of the extracellular domains of the alpha
 CC specificity determining components of their receptors and the
 CC extracellular domain of gp130. The resultant heterodimers, function as
 CC high-affinity traps, rendering the cytokine inaccessible to form a signal
 CC transducing complex with the native membrane-bound forms of their
 CC receptor. The nucleic acids and polypeptides are useful for treating
 CC cytokine-related diseases or disorders such as osteoporosis and primary
 CC and secondary effects of cancer including multiple myeloma or cachexia
 XX
 XX Sequence 1168 AA;
 SQ

Query Match 62.3%; Score 1783; DB 3; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 1.7e-110; Indels 0; Gaps 0;
 Matches 330; Conservative 1; Mismatches 0;
 QY 1 MLAVGCAALAAALAAAGALAPRCPAQEVAVGVLTSLPGDSVTLTLCPGVEPEDNATVHM 60
 DB 1 MVAVGCAALAAALAAAGALAPRCPAQEVAVGVLTSLPGDSVTLTLCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLLRSLVQLHDSGNYSCYRAGRPAAGTVHLLVDVPEBPOL 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLLRSLVQLHDSGNYSCYRAGRPAAGTVHLLVDVPEBPOL 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPFCQYSDSOKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPFCQYSDSOKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAAKPRALSTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQDPDPANITVTVAAKPRALSTWOD 240

Db 181 PEGDSSFFYIVSMCVASVSGSKFSTQTPOGCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLQHCVHIDAMSGLRHVQVLRQAEFFGQ 300
 Db 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLQHCVHIDAMSGLRHVQVLRQAEFFGQ 300
 QY 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331
 Db 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331

RESULT 33
 ABO2177
 ID ABO2177 standard; protein; 1168 AA.
 AC ABO2177;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human cytokine trap-412 protein.
 XX
 DE Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
 KW cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003143697-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 28-OCT-2002; 2002US-00282162.
 XX
 PR 22-SEP-1999; 99WO-US022045.
 PR 22-MAR-2001; 2001US-00787835.
 XX
 PA (STAHL/) STAHL N.
 PA (YANC/) YANCOPOULOS G D.
 PI Stahl N, Yancopoulos GD;
 DR WPI; 2003-851784/79.
 DR N-PSDB; AAD63740.
 XX

PT New nucleic acid molecules encoding fusion polypeptides capable of
 binding a cytokine to form a non-functional complex, useful for treating
 cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 or osteoporosis.
 PT
 PS
 XX
 PS
 XX

Example 8; Fig 24; 300bp; English.

CC The present invention provides a novel fusion polypeptide capable of
 binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human
 CC cytokine trap protein
 CC
 XX
 XX

SQ Sequence 1168 AA;

Query Match 62.3%; Score 1783; DB 7; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 1,7e-110;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTAIVGALLAALAAAGGALAPRCPAOEVARGVLTSLGDSVTLTCTPGVEPEDNATVAM 60
 Db 1 MVAIVGALLAALAAAGGALAPRCPAOEVARGVLTSLGDSVTLTCTPGVEPEDNATVAM 60
 QY 61 VLKRPAGSHPSRWAGGRLLRLSVQLHDSGVSCYRAGRPAGTVHLLVDVPPESPQIS 120
 Db 61 VLKRPAGSHPSRWAGGRLLRLSVQLHDSGVSCYRAGRPAGTVHLLVDVPPESPQIS 120
 QY 121 CFRKSPISNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOBPQYOSQESQGLAV 180
 Db 121 CFRKSPISNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOBPQYOSQESQGLAV 180

Db 121 CFRKSPISNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOBPQYOSQESQGLAV 180
 QY 181 PEGDSSFFYIVSMCVASVSGSKFSTQTPOGCGILQDPDPANITVTVAARNPRLSVTWOD 240
 Db 181 PEGDSSFFYIVSMCVASVSGSKFSTQTPOGCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLQHCVHIDAMSGLRHVQVLRQAEFFGQ 300
 Db 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLQHCVHIDAMSGLRHVQVLRQAEFFGQ 300
 QY 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331
 Db 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331

RESULT 34
 AAO23014
 ID AAO23014 standard; protein; 325 AA.
 AC AAO23014;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Human interleukin 6 receptor alpha chain wild-type peptide.
 XX
 DE Cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV;
 KW nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor; IL-6R;
 KW alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KW rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KW mesangial proliferative glomerulonephritis; Kaposi's sarcoma; poriasis;
 KW osteoporosis; protein co-ordinate data; wild-type.
 XX
 OS Homo sapiens.
 XX

XX
 FH Key
 FT 1..93
 FT /note= "D1 domain"
 FT Domain
 FT 1..5
 FT /note= "dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 6..174
 FT /label= Disulfide_bond
 FT 19..23
 FT /note= "dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 65..69
 FT /note= "dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 93..99
 FT /note= "dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 94..194
 FT /note= "D2 domain"
 FT 94..95
 FT /note= "Double proline motif"
 FT 106..110
 FT /note= "I1 loop"
 FT 118..119
 FT /note= "dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 132..141
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 133..138
 FT /note= "L2 loop"
 FT 160..168
 FT /note= "L3 loop"
 FT 165..169
 FT /note= "SSPY motif"
 FT 166..172
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 179..196
 FT Domain

FT	FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	Domain	190. .193
FT	FT	/note= "L4 loop"
FT	Domain	195. .239
FT	FT	/note= "D3 domain"
FT	Domain	199. .200
FT	FT	/note= "Double proline motif"
FT	Modified-site	226
FT	FT	/note= "N-glycosylated"
FT	Domain	227. .233
FT	FT	/note= "L5 loop"
FT	Domain	227. .230
FT	FT	/note= "SSRF motif"
FT	Domain	233. .239
FT	FT	/label= "Tryptophan-arginine ladder
FT	FT	/note= "Forms a left-handed 310 helix structure"
FT	Domain	241. .250
FT	FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	Domain	244. .248
FT	FT	/label= "Tryptophan-arginine ladder
FT	FT	/note= "Forms a left-handed 310 helix structure"
FT	Domain	250. .256
FT	FT	/note= "L6 loop"
FT	Domain	261. .262
FT	FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	FT	270. .290
FT	Domain	/label= "Tryptophan-arginine ladder
FT	FT	/note= "Forms a left-handed 310 helix structure"
FT	Domain	272. .276
FT	FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	FT	276. .281
FT	Domain	/note= "L7 loop"
FT	FT	282. .290
FT	FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	Domain	284. .287
FT	FT	/note= "WSXWS motif"
FT	Domain	302. .303
FT	FT	/note= "Double proline motif"
PN	WO2003025017-A1.	
PD	27-MAR-2003.	
XX	16-SEP-2002; 2002WO-AU001255.	
XX	14-SEP-2001; 2001AU-00007695.	
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX	(LUDWIG-) LUDWIG INST CANCER RES.	
XX	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
PI	Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM;	
PI	Smith BJ.	
DR	WPI; 2003-558820/52.	
PT	Selecting or designing compound interacting with interleukin receptor,	
PT	useful for treatment of e.g. AIDS, involves assessing and testing	
PT	compound to modulate activity of receptor.	
XX	Disclosure; Page 356-357, 361pp; English.	
XX	The invention relates to selecting or designing a compound that interacts	
CC	with the interleukin-6 receptor (IL-6R) via assessing and obtaining the	
CC	stereochemical complementarity between the compound and a topographic	
CC	region of the receptor and testing the compound for its ability to	
CC	modulate an activity associated with the receptor. Also disclosed is the	
CC	crystal structure of the IL-6R alpha chain. The compounds of the	

CC	invention act as cytokine receptor modulators and may be useful in the prevention and treatment of diseases associated with signalling by IL-6R
CC	such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
CC	prostate cancer, Castleman's disease, AIDS, mesangial proliferative
CC	glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
CC	The method provides enhanced stereochemical complementarity relative to
CC	the naturally occurring IL-6 receptor ligand as well as a rational basis
CC	for the development of ligands for specific therapeutic applications. The
CC	information provided by the IL-6R crystal structure will facilitate a
CC	more accurate understanding of how the binding of a ligand leads to
CC	signal transduction. The current sequence is that of the human IL-6R
CC	alpha chain wild-type protein of the invention
XX	
XX	Sequence 325 AA:
SO	
Query Match	61.6%; Score 1763; DB 7; Length 325;
Best Local Similarity	100.0%; Pred. No. 7.6e-110;
Matches 325;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	20 LARRCPAOGVARGVLTSLGDDSTLTLCPCGPEPBDNATVMVLAKPAPGSHPRWAGMR 79
Db	1 LARRCPAOGVARGVLTSLGDDSTLTLCPCGPEPBDNATVMVLAKPAPGSHPRWAGMR 60
QY	80 RLILRSVQLHDSGNSCYRAGRPAGTVHLVDVPEEPOLSCFRKPSLSNVVCEWGPST 139
Db	61 RLILRSVQLHDSGNSCYRAGRPAGTVHLVDVPEEPOLSCFRKPSLSNVVCEWGPST 120
QY	140 PSLTTKAVLLVRFQNSPAEDFOEPCQYSQESQKFSQCLAVPEGDSISFYISMCAVSSVG 199
Db	121 PSLTTKAVLLVRFQNSPAEDFOEPCQYSQESQKFSQCLAVPEGDSISFYISMCAVSSVG 180
QY	200 SKRSKOTFGCGGILQDPDPANITVTVAARNPRULSTWQDPHNSNSFFYLRLPELRRA 259
Db	181 SKRSKOTFGCGGILQDPDPANITVTVAARNPRULSTWQDPHNSNSFFYLRLPELRRA 240
QY	260 ERSKTFPTMVKDLOHHCVHDAWSGARHVYQLRAOEFQGGSEMSPEAMGTPTESR 319
Db	241 ERSKTFPTMVKDLOHHCVHDAWSGARHVYQLRAOEFQGGSEMSPEAMGTPTESR 300
QY	320 SPPAENEVSTPMQALTTNKDDNLT 344
Db	301 SPPAENEVSTPMQALTTNKDDNLT 325
RESULT 35	
AA70122	
ID	AA70122 standard; protein; 1042 AA.
AC	AA70122;
XX	
XX	16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	14-FEB-1996 (first entry)
XX	
XX	IL6-R type 1-GBP 130 fusion protein.
XX	
KW	Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW	red blood cell; cytokine receptor; Plasmodium falciparum; fusion protein;
KW	GBP 130; GBP1; glycoprotein binding peptide homologue; glycoprotein A.
XX	
OS	Homo sapiens.
OS	Plasmodium falciparum.
OS	Chimeric.
XX	
XX	Key
FT	Misc-difference 54
FT	/label= OTHER
FT	/note= "Arn (sic) "
XX	
PN	W0506737-A1.
XX	
XX	09-MAR-1995.
XX	

PF 01-SEP-1994; 94MO-GB001900.
 XX 03-SEP-1993; 93GB-00018350.
 PR 23-AUG-1994; 94GB-00017021.
 XX (PREN/) PRENDERGAST K F.
 PI Prendergast KF;
 DR WPI; 1995-115452/15.
 XX New hybrid peptide(s) for binding cytokine(s) - comprising a malaria
 FT parasite peptide capable of binding a red blood cell and a receptor
 FT peptide.
 PS Example A; Page 77-78; 93pp; English.

Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood cell
 CC (RBC) and a receptor peptide are claimed. R70103-25 are examples of
 CC these hybrid peptides. R70122 is a fusion of interleukin 6 receptor (as
 CC confirmed with reference to SWISSPROT, as it is unclear in the
 CC specification whether this sequence is IL6-R or IL8-R type1) and
 CC glycoprotein binding protein (GBP) 130. The use of cytokine receptors not
 CC normally found on RBCs means that the cytokine can bind harmlessly to the
 CC RBC without deleterious effect. The RBC protects the hybrid peptides from
 CC excretion from the kidney, and due to steric hindrance prevents the
 CC cytokines binding to a receptor in another cell. GBP 130 or GBPH (GBP
 CC homologue) are the pred. malaria parasite peptides used, others include
 CC BBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite
 CC surface antigen) and the Duffy binding receptor molecule (eg. exhibited
 CC by Plasmodium vivax). These peptides bind to pref. glycoprotein A, B and
 CC C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides
 CC are thus used to lower the levels of free cytokines in the circulation to
 CC reduce pathological damage. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 1042 AA;

XX Query Match 61.5%; Score 1759; DB 2; Length 1042;

XX Best Local Similarity 69.6%; Pred. No. 6e-109; Indels 60; Gaps 10;

XX Matches 362; Conservative 25; Mismatches 73; Indels 60; Gaps 10;

QY 20 LARRCPAQGVNAGVLTSLPGDSVTLTCGVEPEDNATVWYLRKPAAGSHPSRWAGMR 79
 DB 1 LARRCPAQGVNAGVLTSLPGDSVTLTCGVEPEDNATVWYLRKPAAGSHPSRWAGMR 60
 QY 80 RLILRSVQLADSGNYSCTYRAGRPAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEWGPST 139
 DB 61 RLILRSVQLADSGNYSCTYRAGRPAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEWGPST 119
 QY 140 PSLTTKAVLVLRKQNSPADPFOEPCOYSGESQKFCQALAVPGDSSFYIVSMCVASVYG 199
 DB 120 PSLTTKAVLVLRKQNSPADPFOEPCOYSGESQKFCQALAVPGDSSFYIVSMCVASVYG 172
 QY 200 SKFSKTQFQCGILQDPDPANITVIAVANPRLSVTWODPHSNWSSFYRLRFEELRYA 259
 DB 173 SKFSKTQFQCGILQDPDPANITVIAVANPRLSVTWODPHSNWSSFYRLRFEELRYA 232
 QY 260 ERSKFTTMYVYDIQHCVTHDAMSGLRHVQVLRPAQEPFGQSEMSPEAMGTPWTESS 319
 DB 233 ERSKFTTMYVYDIQHCVTHDAMSGLRHVQVLRPAQEPFGQSEMSPEAMGTPWTESS 292
 QY 320 SPPEANVSTPMQALTTKDDNILFRDSANATSLPV-----EFM 359
 DB 293 SPPEANVSTPMQALTTKDDNILFRDSANATSLPVQDNAYICGDYKRAVDYGFRESR 352
 QY 360 PVPPEGDS-----KDVAAHPROPLTSSRRINQRIYILDGISARKETCNKSNWCESSK- 413
 DB 353 ILAEGEDTCARKEKTLTKRSKOK-TSTRTVAIQ-----TKQDENKSVVTEBOKV 401
 QY 414 ELALAEENNLTPMAKRDGFGSGFNEECVIVITGILFEFVYLE-----YLQNR 464

DB 402 ESDSEKQKTKKVVKKQ--INIGDTENQEGKNVKKVKKKKKESGKPEBNKHANEAS 459
 QY 465 ESSEEDARAVQW---STKVLIQFLOKXKONLDAITPDP 500
 DB 460 KKKEPKRSKVSQKRPSTSTRSNNEVKIRASNOETLSADP 499

RESULT 36

AA023016

ID AA023016 standard; protein: 325 AA.

AC AA023016;

DT 17-SEP-2003 (first entry)

DE Human interleukin 6 receptor alpha chain mutant peptide - V259Q.

XX Cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV;
 KW nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor; IL-6R;
 KW alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KW rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KW mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
 KW osteoporosis; protein co-ordinate data; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

FH Key Location/Qualifiers

FT 1..93 /note= "D1 domain"

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /label= Disulfide_bond

FT 19..23 /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

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FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Dimer interface, at which IL-6R monomers interact

FT /note= "Double proline motif"
 FT Modified-site 226
 FT /note= "N-glycosylated"
 FT Domain 227..233
 FT /note= "75 loop"
 FT Domain 227..230
 FT /note= "SSPY motif"
 FT Domain 233..239
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 241..250
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 244..248
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 250..256
 FT /note= "L6 loop"
 FT Misc-difference 259
 FT /note= "Wild-type Val substituted by Gln"
 FT Domain 261..262
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 270..290
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 272..276
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 276..281
 FT /note= "L7 loop"
 FT Domain 282..290
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 284..287
 FT /note= "MSXWS motif"
 FT Domain 302..303
 FT /note= "Double proline motif"
 PN WO2003025017-A1.
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002MO-AU001255.
 XX 14-SEP-2001; 2001AU-00007695.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (LUDWIG INST CANCER RES.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM,
 PI Smith BJ;
 XX MPI; 2003-558820/52.
 DR Selecting or designing compound interacting with interleukin receptor,
 PT useful for treatment of e.g. AIDS, involves assessing and testing
 PT compound to modulate activity of receptor.
 XX
 PS Example 1; Page: 361pp; English.
 XX
 CC The invention relates to selecting or designing a compound that interacts
 CC with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
 CC stereochemical complementarity between the compound and a topographic
 CC region of the receptor and testing the compound for its ability to
 CC modulate an activity associated with the receptor. Also disclosed is the
 CC crystal structure of the IL-6R alpha chain. The compounds of the
 CC invention act as cytokine receptor modulators and may be useful in the
 CC prevention and treatment of diseases associated with signalling by IL-6R
 CC such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
 CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative
 CC glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.

CC The method provides enhanced stereochemical complementarity relative to
 CC the naturally occurring IL-6 receptor ligand as well as a rational basis
 CC for the development of ligands for specific therapeutic applications. The
 CC information provided by the IL-6R crystal structure will facilitate a
 CC more accurate understanding of how the binding of a ligand leads to
 CC signal transduction. The current sequence is that of the human IL-6R
 CC alpha chain mutant protein of the invention which contains a V259Q
 CC substitution. Note: The present sequence is not shown within the
 CC specification but was created by the indexer using the human IL-6R alpha
 CC chain wild-type protein sequence (AA023014)
 XX
 SQ Sequence 325 AA;
 Query Match 61.4%; Score 1757; DB 7; Length 325;
 Best Local Similarity 99.7%; Pred. No. 1.9e-109; Indels 0; Gaps 0;
 Matches 324; Conservative 0; Mismatches 1;
 QY 20 LAERRCPAGEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLKRKPAAGSHPSRMAGMGR 79
 DB 1 LAERRCPAGEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLKRKPAAGSHPSRMAGMGR 60
 QY 80 RLILRSVQLHDSGNSCYRAGRPAGTVHLVDYPPPEPOLSCRRKSPLSNVCEMGRPRST 139
 DB 61 RLILRSVQLHDSGNSCYRAGRPAGTVHLVDYPPPEPOLSCRRKSPLSNVCEMGRPRST 120
 QY 140 PSLTTAVALLVRKFGNSPADPEPCOYSOESOKFCOLAVPEGDSFFYIVSCVASSVG 199
 DB 121 PSLTTAVALLVRKFGNSPADPEPCOYSOESOKFCOLAVPEGDSFFYIVSCVASSVG 180
 QY 200 SKESKTQTFQGGGIILOPPDPANITTVAVARNPRLSVTQDPHSWNSFFYRLRFEILRYRA 259
 DB 181 SKESKTQTFQGGGIILOPPDPANITTVAVARNPRLSVTQDPHSWNSFFYRLRFEILRYRA 240
 QY 260 ERSKTTTMMVVDLQHHCVIHDAMSGLRVYVQLRAQEEGCGMSWSPAMGTPTESR 319
 DB 241 ERSKTTTMMVVDLQHHCVIHDAMSGLRVYVQLRAQEEGCGMSWSPAMGTPTESR 300
 QY 320 SPPAENEVSTPMQALTTNKDDNII 344
 DB 301 SPPAENEVSTPMQALTTNKDDNII 325
 RESULT 37
 AA023018
 ID AA023018 standard; protein; 325 AA.
 XX
 AC AA023018;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Human interleukin 6 receptor alpha chain mutant peptide - C192A.
 XX
 KW Cytostatic; antiinflammatory; antirheumatic; anti-HIV;
 KW nephrotropic; osteoparatic; antipsoriatic; interleukin-6 receptor; IL-6R;
 KW alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KW rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KW mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
 KW osteoporosis; protein co-ordinate data; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..93
 FT /note= "D1 domain"
 FT Domain 1..5
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Disulfide-bond 6..174
 FT /label= "Disulphide_bond"
 FT Domain 19..23
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"

FT Domain 65..69
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 93..99
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 94..194
/note= "D2 domain"
FT Domain 94..95
/note= "Double proline motif"
FT Domain 106..110
/note= "L1 loop"
FT Domain 118..119
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 132..141
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 133..138
/note= "L2 loop"
FT Domain 160..168
/note= "L3 loop"
FT Domain 165..169
/note= "SSFY motif"
FT Domain 166..172
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 179..196
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 190..193
/note= "L4 loop"
FT Domain 192
/note= "Wild-type Cys substituted by Ala"
FT Domain 195..299
/note= "D3 domain"
FT Domain 199..200
/note= "Double proline motif"
FT Modified-site 226
/note= "N-glycosylated"
FT Domain 227..233
/note= "L5 loop"
FT Domain 227..230
/note= "SSFY motif"
FT Domain 233..239
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 241..250
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 244..248
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 250..256
/note= "L6 loop"
FT Domain 261..262
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 270..290
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 272..276
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 276..281
/note= "L7 loop"
FT Domain 282..290
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 284..287
/note= "WSXWS motif"
FT Domain 302..303
/note= "Double proline motif"

XX WO2003025017-A1.
PN 27-MAR-2003.
XX 16-SEP-2002; 2002WO-AU001255.
XX 14-SEP-2001; 2001AU-00007695.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (IUDM-) LUDWIG INST CANCER RES.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM,
PI Smith BJ,
XX WPI; 2003-558820/52.
DR Selecting or designing compound interacting with interleukin receptor,
XX useful for treatment of e.g. AIDS, involves assessing and testing
PT compound to modulate activity of receptor.
PT compound to modulate activity of receptor.
XX Example 1; Page; 361pp; English.
PS The invention relates to selecting or designing a compound that interacts
XX with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
XX stereochemical complementarity between the compound and a topographic
CC region of the receptor and testing the compound for its ability to
CC modulate an activity associated with the receptor. Also disclosed is the
CC crystal structure of the IL-6R alpha chain. The compounds of the
CC invention act as cytokine receptor modulators and may be useful in the
CC prevention and treatment of diseases associated with signalling by IL-6R
CC such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative
CC glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
CC The method provides enhanced stereochemical complementarity relative to
CC the naturally occurring IL-6 receptor ligand as well as a rational basis
CC for the development of ligands for specific therapeutic applications. The
CC information provided by the IL-6R crystal structure will facilitate a
CC more accurate understanding of how the binding of a ligand leads to
CC signal transduction. The current sequence is that of the human IL-6R
CC alpha chain mutant protein of the invention which contains a C192A
CC substitution. Note: The present sequence is not shown within the
CC specification but was created by the indexer using the human IL-6R alpha
CC chain wild-type protein sequence (AA023014)
XX
SQ Sequence 325 Aa;
Query Match 61.3%; Score 1754; DB 7; Length 325;
Best Local Similarity 99.7%; Pred. No. 3.1e-109;
Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 LARRCPAQRVANGVLTSLPGDSVTITLCQVREEDNATYVTLRKPAAGSHPRKMGMR 79
DB 1 LARRCPAQRVANGVLTSLPGDSVTITLCQVREEDNATYVTLRKPAAGSHPRKMGMR 60
QY 80 RLILRSVQLHDSNGSYRAGRPAGTWHLLVDVPEEPOLSCRRKSPLSNVCEMGPRST 139
DB 61 RLILRSVQLHDSNGSYRAGRPAGTWHLLVDVPEEPOLSCRRKSPLSNVCEMGPRST 120
QY 140 PSLLTAAVLLVRKFNQSPAEPOEPCQYSGQSKFCQALVAPGDSFFYIVSMCVASVVG 199
DB 121 PSLLTAAVLLVRKFNQSPAEPOEPCQYSGQSKFCQALVAPGDSFFYIVSMCVASVVG 180
QY 200 SKFSKTQTFQGGGILLDPDPANITTVANANPWLSTYWDPPHSNNSSFRLLRPELRYRA 259
DB 181 SKFSKTQTFQGAAILQPDPPANITTVANANPWLSTYWDPPHSNNSSFRLLRPELRYRA 240
QY 260 ERSKTFTMMWVXKLOHNCVLDHAWSGLRHVYVQLRAOEEFQGMSEWSPAMGTPWTESR 319
DB 241 ERSKTFTMMWVXKLOHNCVLDHAWSGLRHVYVQLRAOEEFQGMSEWSPAMGTPWTESR 300
QY 320 SPFAENEVSTPMQALTTNKDDNLL 344

Db 301 SPPAENEVSTPMQALITNNKDDNII 325

RESULT 38
AAB15389
ID AAB15389 standard; protein; 325 AA.

XX AAB15389;

DT 11-DEC-2000 (first entry)

DE Human interleukin 6 receptor protein.

KM Human interleukin-6 receptor; fungus; *Pichia pastoris*; PCR primer;

XX expression vector; immunoglobulin-like region; cytokine receptor region.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 57 /note= "encoded by GGC"

FT Misc-difference 281 /note= "encoded by CAA"

PN JP2000157280-A.

PD 13-JUN-2000.

PF 26-NOV-1998; 98JP-00335464.

PR 26-NOV-1998; 98JP-00335464.

PA (TOYO) TOSOH CORP.

XX WPI; 2000-468203/41.

DR N-PSDB; AAA70701.

XX Yeasts transformed with IL-6 receptor gene.

PS Example 1; Page 6-8; 10pp; Japanese.

CC The invention relates to the production of human interleukin-6 receptor
CC (IL-6R) protein in the fungus *Pichia pastoris*. The fungus was transformed
CC with an expression vector (pOIC3-420UL) containing a gene encoding an IL-
CC 6R protein having an immunoglobulin-like region and cytokine receptor
CC region and spanning amino acids from Leu20-Ala323. The human IL-6R region
CC was PCR amplified using the primers AAA70702-A70703. This sequence
CC represents the recombinant IL-6R protein of the invention
XX

SO Sequence 325 AA;

Query Match 61.1%; Score 1748; DB 3; Length 325;

Best Local Similarity 99.4%; Pred. No. 7.7e-109; Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 LARRRCPADEVAVAGVLTSLPGDSVTLTCTGVEPEDNATVMVLRKPAAGSHPRMAMGMR 60

QY 20 LARRRCPADEVAVAGVLTSLPGDSVTLTCTGVEPEDNATVMVLRKPAAGSHPRMAMGMR 79

Db 80 RLILRSVQLHDSGNVSCYRAGRAGTVHLVDPPEEPOLSCFRKSPLSNVVCEMGPRT 139

QY 61 RLILRSVQLHDSGNVSCYRAGRAGTVHLVDPPEEPOLSCFRKSPLSNVVCEMGPRT 120

Db 140 PSILTTAVALLVRKFQNSPADPFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 180

QY 121 PSILTTAVALLVRKFQNSPADPFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 199

Db 200 SKSKSTQTFQGGCIILOPDPANITTVAVANRPMWLSVTWODPHSNMSSFRRLRFEELRYRA 259

QY 181 SKSKSTQTFQGGCIILOPDPANITTVAVANRPMWLSVTWODPHSNMSSFRRLRFEELRYRA 240

Db 260 ERSKFTTMMVVKDLOHHCVIHDAMSGLRHVVOQLRAQEEFGGSEMSSEPMAGTPTWTSR 319

Db 241 ERSKFTTMMVVKDLOHHCVIHDAMSGLRHVVOQLRAQEEFGGSEMSSEPMAGTPTWTSR 300

QY 320 SPPAENEVSTPMQALITNNKDDNII 344

Db 301 SPPAENEVSTPMQALITNNKDDNII 325

RESULT 39
AAB15390
ID AAB15390 standard; protein; 325 AA.

XX AAB15390;

DT 15-DEC-2000 (first entry)

DE Bovine interleukin-12 p35 subunit protein.

KM Anticardiotonic; bovine; interleukin 12; IL12; heterodimer; infection.

XX Bos taurus.

PN JP2000157274-A.

PD 13-JUN-2000.

PF 20-NOV-1998; 98JP-00331052.

PR 20-NOV-1998; 98JP-00331052.

PA (DAUC) DAICHI PHARM CO LTD.

XX WPI; 2000-468201/41.

DR N-PSDB; AAA70708.

XX Preparation of bovine interleukin 12 comprising using a vector containing
PT the gene encoding it, useful for the prevention and treatment of chronic
PT and opportunistic infections.

PS Example 1; Page 8; 11pp; Japanese.

CC The invention relates to a method for the preparation of bovine
CC interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC vectors containing genes encoding the p35 and p40 subunits. This sequence
CC represents the bovine IL12 p35 subunit. Interleukin 12 is used for the
CC prevention and treatment of chronic infections and opportunistic
CC infections
XX

SO Sequence 325 AA;

Query Match 61.1%; Score 1748; DB 3; Length 325;

Best Local Similarity 99.4%; Pred. No. 7.7e-109; Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 LARRRCPADEVAVAGVLTSLPGDSVTLTCTGVEPEDNATVMVLRKPAAGSHPRMAMGMR 60

QY 20 LARRRCPADEVAVAGVLTSLPGDSVTLTCTGVEPEDNATVMVLRKPAAGSHPRMAMGMR 79

Db 80 RLILRSVQLHDSGNVSCYRAGRAGTVHLVDPPEEPOLSCFRKSPLSNVVCEMGPRT 139

QY 61 RLILRSVQLHDSGNVSCYRAGRAGTVHLVDPPEEPOLSCFRKSPLSNVVCEMGPRT 120

Db 140 PSILTTAVALLVRKFQNSPADPFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 180

QY 121 PSILTTAVALLVRKFQNSPADPFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 199

Db 200 SKSKSTQTFQGGCIILOPDPANITTVAVANRPMWLSVTWODPHSNMSSFRRLRFEELRYRA 259

QY 181 SKSKSTQTFQGGCIILOPDPANITTVAVANRPMWLSVTWODPHSNMSSFRRLRFEELRYRA 240

Db 260 ERSKFTTMMVVKDLOHHCVIHDAMSGLRHVVOQLRAQEEFGGSEMSSEPMAGTPTWTSR 319

Db 241 ERSKTTTMMVKDLQHHCIVIHDAWSGLRHVVQJRAQEEFGGSMSEKSPAMGTPWTESR 300
 QY 320 SPPAENEVSTPMQALTTNKDDNIL 344
 Db 301 SPPAENEVSTPMQALTTNKDDNIL 325

RESULT 40
 AAO23015
 ID AAO23015 standard; protein; 325 AA.
 AC AAO23015;
 XX
 XX 17-SEP-2003 (first entry)
 DE Human interleukin 6 receptor alpha chain mutant peptide - W214N.
 XX Cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV;
 KM nephrotropic; osteopathic; antipneumatic; interleukin-6 receptor; IL-6R;
 KM alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KM rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KM mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
 KM osteoporosis; protein co-ordinate data; mutant; mutein.
 XX
 OS Homo sapiens.
 SX Synthetic.
 FH Key
 FT Location/Qualifiers
 FT 1..93
 FT /note= "D1 domain"
 FT Domain
 FT 1..5
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Disulfide-bond
 FT 6..174
 FT /label= Disulphide_bond
 FT 19..23
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain
 FT 65..69
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 93..99
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain
 FT 94..134
 FT /note= "D2 domain"
 FT 94..95
 FT /note= "Double proline motif"
 FT 106..110
 FT /note= "L1 loop"
 FT 118..119
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain
 FT 132..141
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain
 FT 133..138
 FT /note= "L2 loop"
 FT 160..168
 FT /note= "L3 loop"
 FT 165..169
 FT /note= "SSFY motif"
 FT 166..172
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT 179..196
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain
 FT 190..193
 FT /note= "L4 loop"
 FT 195..299
 FT /note= "D3 domain"
 FT 199..200
 FT Domain

FT /note= "Double proline motif"
 FT Misc-difference 214
 FT /note= "Wild-type Trp substituted by Asn"
 FT Modified-site 226
 FT /note= "N-glycosylated"
 FT Domain 227..233
 FT /note= "L5 loop"
 FT Domain 227..230
 FT /note= "SSFY motif"
 FT Domain 233..239
 FT /label= Tryptophan-arginine_ladder
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 241..250
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 244..248
 FT /label= Tryptophan-arginine_ladder
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 250..256
 FT /note= "L6 loop"
 FT Domain 261..262
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 270..290
 FT /label= Tryptophan-arginine_ladder
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 FT /note= "Dimer interface, at which IL-6R monomers interact
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 FT /note= "L7 loop"
 FT Domain 282..290
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 284..287
 FT /note= "WSXWS motif"
 FT Domain 302..303
 FT /note= "Double proline motif"
 FT
 FT W02003025017-A1.
 XX
 XX 27-MAR-2003.
 XX
 XX 16-SEP-2002; 2002MO-AU001255.
 XX
 XX 14-SEP-2001; 2001AU-00007695.
 XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.
 XX
 XX Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM;
 XX Smith BJ;
 XX WPI; 2003-558820/52.
 XX
 XX Selecting or designing compound interacting with interleukin receptor,
 XX useful for treatment of e.g. AIDS, involves assessing and testing
 XX compound to modulate activity of receptor.
 XX
 XX Example 1; Page; 361pp; English.
 XX
 XX The invention relates to selecting or designing a compound that interacts
 XX with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
 XX stereochemical complementarity between the compound and a topographic
 XX region of the receptor and testing with the compound for its ability to
 XX modulate an activity associated with the receptor. Also disclosed is the
 XX crystal structure of the IL-6R alpha chain. The compounds of the
 XX invention act as cytokine receptor modulators and may be useful in the
 XX prevention and treatment of diseases associated with signalling by IL-6R
 XX such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
 XX prostate cancer, Castleman's disease, AIDS, mesangial proliferative
 XX glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
 CC

CC The method provides enhanced stereochemical complementarity relative to
CC the naturally occurring IL-6 receptor ligand as well as a rational basis
CC for the development of ligands for specific therapeutic applications. The
CC information provided by the IL-6 crystal structure will facilitate a
CC more accurate understanding of how the binding of a ligand leads to
CC signal transduction. The current sequence is that of the human IL-6R
CC alpha chain mutant protein of the invention which contains a W214N
CC substitution. Note: The present sequence is not shown within the
CC specification but was created by the indexer using the human IL-6R alpha
CC chain wild-type protein sequence (AA023014)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:55:07 ; Search time 47.8543 seconds
(without alignments)
1091.766 Million cell updates/sec

Title: US-09-462-416-7
Perfect score: 2861
Sequence: 1 MNAVCAALALALAAFGAL.....LILRSFKETLQSLRALRQM 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1918	67.0	468	1 A41242	interleukin-6 rece
2	954.5	33.4	440	2 J10144	interleukin-6 rece
3	954.5	33.4	460	2 J10145	interleukin-6 rece
4	938.5	32.8	212	1 IVDH2	interleukin-6 prec
5	853	29.8	462	1 A37986	interleukin-6 rece
6	571.5	20.0	208	2 T09216	interleukin-6 prec
7	559.5	19.6	212	2 I46621	prointerleukin 6 -
8	557.5	19.5	212	2 I46590	interleukin 6 - pl
9	476	16.6	207	1 A56610	interleukin 6 - ca
10	471	16.5	208	1 A56610	interleukin-6 prec
11	465	16.3	208	1 S29549	interleukin-6 - sh
12	396.5	13.9	211	2 A34247	interleukin-6 prec
13	374.5	13.1	211	1 ICM86	interleukin-6 prec
14	337	11.8	432	2 I48343	interleukin-11 rec
15	330.5	11.6	422	2 I37891	interleukin-11 rec
16	310	10.8	372	2 I58141	ciliary neurotroph
17	306.5	10.7	362	2 S60614	growth promoting a
18	301	10.5	372	1 UHHCN	ciliary neurotroph
19	226	7.9	53	2 I53394	soluble interleuk
20	198.5	6.9	328	2 A38957	interleukin 12b pr
21	180	6.3	831	2 J01655	prolactin receptor
22	178.5	6.2	830	2 I50455	prolactin receptor
23	171	6.0	917	2 I45971	prolactin receptor
24	167.5	5.9	917	2 I45969	glycoprotein 130 -
25	167.5	5.9	918	2 A36337	membrane glycoprot
26	166	5.8	918	2 A44257	interleukin-6 sign
27	161.5	5.6	616	2 A30304	prolactin receptor
28	159	5.6	310	2 A29884	prolactin receptor
29	159	5.6	412	2 A41070	prolactin receptor

30	159	5.6	610	2 A34631	lactogen receptor
31	159	5.6	610	2 A36116	prolactin receptor
32	158.5	5.5	335	2 I72789	interleukin 12 p40
33	158	5.5	630	2 I51086	prolactin receptor
34	155	5.4	292	2 I77525	prolactin receptor
35	155	5.4	303	2 I77524	prolactin receptor
36	155	5.4	608	2 I53269	prolactin receptor
37	146	5.1	890	1 A53743	protein-tyrosine k
38	144	5.0	1896	2 T08851	Down syndrome cell
39	138	4.8	288	2 B59405	prolactin receptor
40	138	4.8	376	2 A59405	prolactin receptor
41	138	4.8	622	2 A40144	prolactin receptor
42	137.5	4.8	882	2 I36912	receptor tyrosine
43	134.5	4.7	895	2 S74225	leptin receptor, 1
44	133.5	4.7	837	2 A34898	granulocyte colony
45	133.5	4.7	880	1 J04166	protein-tyrosine k

ALIGNMENTS

RESULT 1

A41242
interleukin-6 receptor precursor - human
N:Contains: interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C>Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashita, Y.; Seed, B.; Taniguchi, T.;
Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A:Reference number: A41242; MUID:88305347; PMID:3136546
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: UNIPROT:P08887; GB:M20566; NID:G33845; PID:CAA31312.1; PID:G33846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashita, Y.; Seed, B.; Taniguchi, T.;
Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
R:Schoellkopf, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, B.;
Biochem. J. 277, 659-664, 1991
A:Title: Structural and functional studies on the human hepatic interleukin-6 receptor.
A:Reference number: S17468; MUID:91336983; PMID:1872801
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:X58298; NID:G32580; PID:CAA41231.1; PID:G32581
A:Experimental source: hepatoma cell line HepG2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; MUID:90010793; PMID:2529343
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, and d
C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetic:
A:Gene: GDB:IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1921-1921
C:Superfamily: Ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-468/Product: interleukin-6 receptor #status predicted <EXT>
F:20-363/Domain: extracellular #status predicted <EXT>
F:40-96/Domain: immunoglobulin homology <IMM2>
F:121-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TM>

F:387-468/Domain: intracellular #status predicted <INT>
F:47-96/Disulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 67.0%; Score 1918; DB 1; Length 468;
Best Local Similarity 96.5%; Pred. No. 2,8e-125;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
QY 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
DB 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 180
DB 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 240
DB 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 240
QY 241 PHSNMSFFYRLRFEELRYAERSKFTTMMVVDLQHCYIHDAMGRLRHVVQLRAQEEFQG 300
DB 241 PHSNMSFFYRLRFEELRYAERSKFTTMMVVDLQHCYIHDAMGRLRHVVQLRAQEEFQG 300
QY 301 GEMSEMSPEAMQTPTESSRPAPENEVSTPMQALITTKDDNLIIFRDSANATSLPVEF 360
DB 301 GEMSEMSPEAMQTPTESSRPAPENEVSTPMQALITTKDDNLIIFRDSANATSLPVEF 360
QY 361 VPPEGDSKDVAAAP 373
DB 357 ----QDSSSVPLP 365

RESULT 2
JL0144
Interleukin-6 receptor precursor (clone lambda p1) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J010144
R/Sugita, T.; Torisaka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A/Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A/Reference number: J010144; MUID:90278354; PMID:2112585
A/Accession: J010144
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-440 <SUG>
A/Cross-references: UNIPROT:P22272; GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
C/Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-440/Product: interleukin-6 receptor #status predicted <SIG>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 33.4%; Score 954.5; DB 2; Length 440;
Best Local Similarity 50.1%; Pred. No. 1.5e-58;
Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
QY 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
DB 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 180
DB 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 180

||||| : ||||| ||||| : : ||||| ||||| : ||||| :
117 CFRKNPLVNAICWRBPSSTPSPTTKAVLLPAKINTNKGSDPQVPCQYQSQKFSQCLAV 176

QY 180 VPPEGDSFFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 239
DB 180 VPPEGDSFFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 239

177 ILBGDKYTHIVSLCVANSGSKSHNEAFHSLKMQVDPDPANLVSAIIGRRMRKVSQ 236
QY 240 DPHSNMSFFYRLRFEELRYAERSKFTTMMVVDLQHCYIHDAMGRLRHVVQLRAQEEFQG 299
DB 240 DPHSNMSFFYRLRFEELRYAERSKFTTMMVVDLQHCYIHDAMGRLRHVVQLRAQEEFQG 299

237 HPETWPSYVLLQFQRLRYPWMSKEFTVLLLPVAGYQCVIHDALGVKHVVQVRKEEHD 296
QY 300 GEMSEMSPEAMQTPTESSRPAPENEVSTPMQALITTKDDNLIIFRDSANATSLPVEF 358
DB 300 GEMSEMSPEAMQTPTESSRPAPENEVSTPMQALITTKDDNLIIFRDSANATSLPVEF 358

297 LGQMSSESPSVGTGTPPIAEPRTTPA-GILMNPQVSVSDSANHEDQYESSTEATSV---- 351
QY 359 MPVPPEGDSKDVAAAP 373
DB 352 --LAPVQESSMSLP 364

RESULT 3
JL0145
Interleukin-6 receptor precursor (clone lambda 301) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J010145; S14543
R/Sugita, T.; Torisaka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A/Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A/Reference number: J010145; MUID:90278354; PMID:2112585
A/Accession: J010145
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-460 <SUG>
A/Cross-references: UNIPROT:P22272; GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
A/Experimental source: clone lambda 301
R/Fiorillo, M.T.; Ciliberto, G.; Dentle, L.
submitted to the EMBL Data Library, July 1990
A/Description: Cloning and expression of murine IL-6 receptor.
A/Reference number: S14543
A/Accession: S14543
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-373, 'R', 375-460 <PIO>
A/Cross-references: EMBL:X53802; NID:952692; PIDN:CAA37810.1; PID:952693
C/Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 33.4%; Score 954.5; DB 2; Length 460;
Best Local Similarity 50.1%; Pred. No. 1.6e-58;
Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
QY 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
DB 61 VLRKPAAGSHPRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAGTVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSPTTKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 179
DB 121 CFRKSPLSNVCEMGPSTPSPTTKAVLLVRKFQNSPADPQEPQOYQESQKFSQCLAV 179
QY 180 VPPEGDSFFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 239
DB 180 VPPEGDSFFYIVSMCVASVSGSKFKTQTFQGGIILQDPDPANITVTAVANRPMILSVTMOD 239
QY 177 ILBGDKYTHIVSLCVANSGSKSHNEAFHSLKMQVDPDPANLVSAIIGRRMRKVSQ 236
DB 177 ILBGDKYTHIVSLCVANSGSKSHNEAFHSLKMQVDPDPANLVSAIIGRRMRKVSQ 236

R;Orita, T.; Oheda, M.; Hasegawa, M.; Kubonliwa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 prod
 A:Reference number: JX0305; MUID:94266765; PMID:8206884
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R;Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human granu
 A:Reference number: S04981; MUID:89286115; PMID:2472117
 A:Contents: annotation; disulfide bonds in recombinant protein
 R;Rock, F.L.; Li, X.; Cheng, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044; PMID:8172889
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor
 C:Comment: This protein plays a regulatory role in various host defense mechanisms and e
 C:Genetics:
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Intons: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth fa
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-212/Product: interleukin-6, long form #status experimental <MATL>
 F;30-212/Product: interleukin-6, short form #status experimental <MATS>
 F;72-78,101-111/Disulfide bonds: #status experimental
 F;73/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental
 F;166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F;172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.8%; Score 938.5; DB 1; Length 212;
 Best Local Similarity 97.9%; Pred. No. 7.2e-58;
 Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MVPPEGSDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCESS 412
 Db 22 LPAAFPAPVPPGEDSKOVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCESS 81

QY 413 KEALAEENNLNLPKAEKDCGFGFNEETCLVKITGLLEFEVYLYETLQNRPFSSSEQAR 472
 Db 82 KEALAEENNLNLPKAEKDCGFGFNEETCLVKITGLLEFEVYLYETLQNRPFSSSEQAR 141

QY 473 AVOMSTKVLIOPLQKAKNDAITTPDPTNASTLTQLQONOWLODMTHLILRSFKER 532
 Db 142 AVOMSTKVLIOPLQKAKNDAITTPDPTNASTLTQLQONOWLODMTHLILRSFKER 201

QY 533 LQSSSLRALROM 543
 Db 202 LQSSSLRALROM 212

RESULT 5
 A37986
 Interleukin-6 receptor precursor - rat
 N:Alternate names: IL-6 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A37986
 R;Baumann, M.; Baumann, H.; Fey, G.H.
 J. Biol. Chem. 265, 19853-19862, 1990
 A>Title: Molecular cloning, characterization and functional expression of the rat liver
 A:Reference number: A37986; MUID:91060602; PMID:2174054
 A:Accession: A37986
 A:Molecule type: mRNA
 A:Residues: 1-462 <BAU>
 A:Cross-references: UNIPROT:P22273; GB:MS8587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
 C:Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is es
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C:Keywords: acute phase; cytokine receptor; transmembrane protein
 F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-462/Product: interleukin-6 receptor #status predicted <MAT>
 F;20-362/Domain: extracellular #status predicted <EXT>
 F;40-99/Domain: immunoglobulin homology <IMM>
 F;117-306/Domain: cytokine receptor homology <CRS>
 F;363-385/Domain: transmembrane #status predicted <TM>
 F;386-462/Domain: intracellular #status predicted <INT>
 F;47-92/Disulfide bonds: #status predicted

Query Match 29.8%; Score 853; DB 1; Length 462;
 Best Local Similarity 48.4%; Pred. No. 1.7e-51;
 Matches 181; Conservative 50; Mismatches 119; Indels 24; Gaps 8;

QY 1 MLAVGALIAALIAAPGALAPRCPAQQVAVGLTSLPGSDVTLLCPGVEEDNATVAM 60
 Db 1 MLAVGTLIVALLAARAVALLVSGCALEAVANGVTSLPGAVITLLCPKEAAGNATTIM 60

QY 61 VLKRPAGSHPSRWAGMRRLIRSVQLHDSGNSCYRAGRAGVYHLIVDPPEBPOLS 120
 Db 61 VY----SGSQSRWMTTGNITLVLRVAVQVNDTGHYLCFLDDHVGTVPLIVDPPEBPOLS 116

QY 121 CPEKSPLSNVGCEWGRSPSLITTKAVLLVRKQNSPAE-DROEPCQYSGESQKSCOLA 179
 Db 117 CPEKNPVNAFCBWHSPSTPSTTKAVMPAKKINTNGSKSDQVPCQYSQULKSFSCEVE 176

QY 180 VPEGDSFYIVSMCVASVSGSKFKTQTPQGGGIIQDPDPANITVAVARN-----PR 232
 Db 177 ILEGDKVYHIVGLCVANSVGSNSHNHVQSLKMQVDPDPALVVASLIGSLVGSKSVGK 236

QY 233 WLSTVWQDPHSMNNSYRLRFEFLRRAERSKFTTMMVKDLOHHCYIHDAMGGLRHVQL 292
 Db 237 TISPQTQVTTCCNSSPDTLVGQR-----FTVWPLQVAOHQCVIHDALGVKGVVQV 289

QY 293 RAQEEFGCEGSEWSEPAAGTPW-TESRSPAPENEVSFPMALTTNKDDNLLFPDSANA 351
 Db 290 KGEKEFDIOMSKMSEPTVGTPLAEPRTTPA-GIPGNFTQVSVDYDHEQDQGSSTBA 348

QY 352 TSL--PVE-FMVPV 362
 Db 349 TSVLAVQGSSPLP 362

RESULT 6
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T09216
 R;Swiderski, C.E.; Horchov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <SWT>
 A:Cross-references: UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: interleukin-6
 C:Keywords: cytokine; growth factor

Query Match 20.0%; Score 571.5; DB 2; Length 208;
 Best Local Similarity 58.5%; Pred. No. 1.9e-32;
 Matches 113; Conservative 32; Mismatches 41; Indels 7; Gaps 3;

QY 351 ANSLPVEFPVPPGEDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCE 410
 Db 23 ANSLPVEFPVPPGEDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCE 76

QY 411 SSKKALAEENNLNLPKAEKDCGFGFNEETCLVKITGLLEFEVYLYETLQNRPFSSSEQ 470
 Db 77 NKKEYLAENNLNLPKAEKDCGFGFNEETCLVKITGLLEFEVYLYETLQNRPFSSSEQ 136

QY 471 ARAVOMSTKVLIOPLQKAKNDAITTPDPTNASTLTQLQONOWLODMTHLILRSFKER 530

Query Match	16.5%;	Score 471;	DB 1;	length 208;
Best Local Similarity	51.6%;	Pred. No. 1.7e-25;		
Matches	94;	Conservative 33;	Mismatches 51;	Indels 4; Gaps 2
Qy	360	PVPPGSDSKDVAAPHROPLVTSSERIDKOIRYLIDGISALRKETCNKSNMCESSKEALAEIN	419	
Db	29	PGSLGDFPNDDTPPGRLITLTPEKTEALIKRWVLDKISMRKEICEKDECESSKETLAEIN	88	
Qy	420	NLNLPRMAKKDCGFOSGFNEETCYWKIITGLLEFVLYEYIÖNNFESSSEQAAVOMSTK	479	
Db	89	KNLPRMEERDCGFOSGFNQALCLRTTAGLEIYQIYIDYIÖNIEBGNÖENVDIKRINIR	148	
Qy	480	VLIQFQKAKNLDATTPDPTTNASLITKLOAQONÖMLQDMTHLILRSFKEPLQSSLR	539	
Db	149	TLIQIL--KQKIALDITTT--PATNIDDLKKQSSNEMVKNKAILILIRNLLENFQESLRA	204	
Qy	540	LR 541		
		:		
Db	205	IR 206		
		:		

RESULT 11
S29549
interleukin-6 - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S29549
R/Ebrahim, B.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29549
A/Accession: S29549
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-208 <ERR>
A/Cross-references: UNIPROT:P29455; EMBL:X68723
C/Superfamily: interleukin-6

[illegible]

RESULT 12

A34247
interleukin-6 precursor - rat
N/Alternate names: IL-6
C/Species: Rattus norvegicus (Norway rat)
C/Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34247
J/Northernmann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
U. Biol. Chem. 264, 16072-16082, 1989
A/Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derived
A/reference number: A34247; PMID:89380206; PMID:2789217
A/Accession: A34247
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-211 <NR>

Query Match
Best Local Similarity 16.3%; Score 465; DB 1; Length 208;
Matches 92; Conservative 34; Mismatches 52; Indels 4; Gaps 2;

Dy 360 PVPPEDESKDVAAPHROPLTSSERRDKQIRYLIDGISTLRKTCNKSNCESSKEALAE 419
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
29 PGLGEDPKNDTPSRLLITPKEIKAIKVDSIKSRIEIEKNDECNSKETLAEN 88
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
420 NINLPKMAEKDCFCFSGFNEETCTVKIITGLLEFEVYLEYQNPFESSEQAARAVONSTK 479
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 KTKLPRMEKKGCCFGSGNQAVCLIKTTAGLLEYQIVDFIQNFEGEQETVMELQSSIR 148
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 480 VLIQTLQKKAKKLDAITPPDPPTNASLTITKOQONQMOMDTHTLILRFPKFLOSSIRA 539
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 TLIIQLIKEKIAGL--ITT--PATHTDLLEKQSSNEWKNAKVITILKSLENLFQFLRA 204
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 540 LR 541
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 IR 206

RESULT 13

ICMS6
Interleukin-6 precursor - mouse
N/Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyt
acytoma growth factor
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: A30531; A27610; A30573; S01323; S12103; E34047; A26662; A40486; A60799; S10;
R/Tanabe, O.; Akita, S.; Kamitani, Y.
J. Immunol. 141, 3875-3881, 1988
A/Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
A/reference number: A30531; PMID:89035525; PMID:3263433
A/Accession: A30531
A/Molecule type: DNA
A/Residues: 1-211 <TA>
A/Cross-references: UNIPROT:P08505; GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386
A/Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Slomg
Eur. J. Immunol. 18, 193-197, 1988
A/Title: cDNA cloning of murine interleukin-HPI: homology with human interleukin 6.
A/reference number: A27610; PMID:88166883; PMID:2965020
A/Accession: A27610
A/Molecule type: mRNA
A/Residues: 1-211 <TA>
A/Cross-references: GB:X06203; NID:g52701; PIDN:CMA29560.1; PID:g52702
J/Mock, B.A.; Nordam, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Clat
R. Immunol. 142, 1372-1376, 1989
A/Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A/reference number: A30571; PMID:89124383; PMID:2563387
A/Accession: A30571
A/Molecule type: mRNA
A/Residues: 5-211 <MO>
A/Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R/Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A/Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and re
A/reference number: S01323; PMID:88329059; PMID:3262059
A/Accession: S01323
A/Molecule type: protein
A/Residues: 25-166 'X', 168-211 <SIM>
A/Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
R/Grenelt, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A/Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A/reference number: S12103; PMID:91057159; PMID:2243807
A/Accession: S12103
A/Molecule type: mRNA
A/Residues: 1-211 <GR>
A/Cross-references: EMBL:X54542; NID:g52727; PIDN:CMA38411.1; PID:g52728

J. Jahnke, W. J. Ward, L. D. Reid, G. E. Moritz, R. L. Simpson, R. J. Biochem. Biophys. Res. Commun. 166: 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Reference number: A90157; MUID:90147691; PMID:2302197
 A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75, 78-94, 128-148 <NA>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoeve, C.; Coulie, P.G.; Rubira, M.R.; Simpson, N. L. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Reference number: A26662; MUID:87092311; PMID:2948184
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulden, C.; Coffman, R.L.; Rennick, D.; Lee, F. Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A40486; MUID:89017145; PMID:3262872
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:003783; NID:G198367; PIDN:AAA9301.1; PID:G309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S. Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753; PMID:3284198
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T. J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mouse myeloma cell line
 A:Reference number: S10241; MUID:90171860; PMID:2106569
 A:Accession: S10241
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:G49738; PIDN:CA53824.1; PID:G581860
 R:Zhang, Y.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J. Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin-6
 A:Reference number: S38254; MUID:94039075; PMID:8225366
 A:Accession: S38254
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60, 75, 'X', 77-79, 176-203 <ZHA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:1-24/Domin: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 C:Gene: IL-6
 A:Map position: 5
 A:Intons: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F:

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Db      199  EFLKVLTRSTQ 210

RESULT 14
148343
interleukin-11 receptor alpha-chain precursor - mouse
N:Alternate names: cytokine type 1 receptor
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #ext_change 09-Jul-2004
C:Accession: 148343; 551619
R:Neuhaus, H.; Betenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossler
Dev. Biol. 166, 521-542, 1994
A:Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryogen
A:Reference number: 148343
A:Accession: 148343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
A:Cross-references: UNIPROT:064385; EMBL:X74953; NID:9673437; PID:CA52908.1; PID:967343
R:Hilton, D.J.; Hilton, A.A.; Ratcevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.; E
EMBO J. 13, 4765-4775, 1994
A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high e
A:Reference number: 551619; MUID:95045367; PMID:7957045
A:Accession: 551619
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432 <HIL>
A:Cross-references: EMBL:U14412; NID:9576454; PID:AAA53248.1; PID:9576455
C:Genetics:
A:Gene: Et12/Il11
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C:Keywords: cytokine receptor
F:120-310/Domain: cytokine receptor homology <CRS>

Query Match      11.8%; Score 337; DB 2; Length 432;
Best Local Similarity 28.0%; Pred. No. 8.7e-16;
Matches 115; Conservative 52; Mismatches 165; Indels 78; Gaps 17;

QY      2  LAVGCALIAALIAIPGAL--APRRCPAQEVARGVLTSLPDSVTLTCGPVEPEDNATVH 59
Db      1  MSSCSGLTRVLVAVATLVSSSSPCQAMGPPGVYQGPGRPVMLCCPGV----- 51
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      60  VWLKRPAAGSHPSR-----AGMRRLILRSYQLHDSGNYSCYRA-GRPAGT 105
Db      52  -----SAGT-FVSNFRDGSRLLOGPDSGLGRLVLAQVSDPEGTYVQTLDGVSQM 104
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      106  VHLVDVPEEPOLSCFRKPSLSNVCEWGPSTPELTTKAVLVLRFKQSPADPOE-- 163
Db      105  VTLKIGFPAPREVSC-QAVDYENFSCTWSFGVSGILPRYLITSYRKKTIPGAEQSRES 163
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      164  -----PCYOSESQKFSQCLAVPEGDS--SFYIVSMCVASSVSGSKSTQTFQGC----- 211
Db      164  STGPPPC-----PQDPLASRCVVGAEFWSEYRINTVENPLG-----STCLDVR 211
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      212  --GIIQPPRPANITVTAARPRMISVTWQDPHSW-NSSTYRLRFELRYAERSKTTTW 268
Db      212  LQSIIRPDPQGLRVSVPGRYRRLHASTVYPSMRQPFILKFLKRLQYRAPAHPAMST- 270
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      269  MYKDLQHCIVLHDASGLRHVVQLAQAEFGCGEWSPEAMGTPTESRSPPAENHVS 328
Db      271  -VEPLGLEEVLTDAVAGLPHAVRSARDLADGTWAMSSEANGTST--GPLQDEI- 324
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      329  TPMQALTNKDDNILFRDSANATSLPVEFMPPSPEDSKDVAAPHROP 378
Db      325  -PDSGCGGQGLEAVVAQEDSPAPARP-SLQDPDRRLD-----HRDPL 365
      :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 15
137891
interleukin-11 receptor alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #ext_change 09-Jul-2004
C:Accession: 137891; G01970; G01971

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A:Accession: I59141
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-572 <IN>
A:Cross-references: UNIPROT:Q08406; GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R:Clatterbuck, R.E.; Price, D.L.; Koliatatos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A>Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cerebellum
A:Reference number: A47387; MUID:93211934; PMID:8460125
A:Accession: A47387
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 185-260,'D',262-277 <CIA>
A:Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A:Experimental source: Sprague-Dawley, brain
A>Note: Sequence extracted from NCBI Backbone (NCBIN:128471, NCBI:P.128472)
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin domain; growth factor receptor
C:Keywods: growth factor receptor
F:39-91/Domain: immunoglobulin homology <IMM>
F:116-296/Domain: cytokine receptor homology <CRS>

Query Match      10.8%; Score 310; DB 2; Length 372;
Best Local Similarity 29.8%; Pred. No. 5.3e-14;
Matches 113; Conservative 46; Mismatches 146; Indels 74; Gaps 17;

Oy      11 ALLAPGALLAPRCPAOEVARGVLTSLPGSVTLTCPGVEPEDNATVHWLRKPAAGSH 70
        ||||| : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      11 AVLAANAAYTTGGHSGQE-AAPHQYERLGIQDTVLPC-GTASND-AAVTWRVN----GTD 63

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[illegible]

Query Match 10.7%; Score 306.5; DB 2; Length 362;
 Best Local Similarity 29.4%; Pred. No. 8.9e-14;
 Matches 100; Conservative 47; Mismatches 128; Indels 65; Gaps 16;

QY 40 GDSVTLTCGVEPEDNATVHWLVRKPAAG-----SHPSRWAGGRLLRSVOLHDSGNY 94
 DB 37 GADVTMKCGSMDW--AAVTWT-----ANGTIDIDSHLN-----GSYLILKNVDLTGSGY 85
 QY 95 SCTYRAG--RPACTVHLVDVPEEPQLSCFRKSPLSNVCEWGRPRSTPBLTKAVILVVK 152
 DB 86 SCYEGSSWHLKXQYTLRVGVPPKPEVLMCRSNYPKGYCSW--HLPGPT-----YIPNS 138
 QY 153 FQNSPADPOEPQCYQSQSCQALAVEGDSF-YIVSMCVASSVGSKFSKTQFGQC 211
 DB 139 FVISTYIHGRENVCEKDITPKRCHRIYQLSTVYKXKTLVYTNALG-KNSTLTITDFEF 197
 QY 212 GILQDPDPANITVTAVARNPRLSVTQDPHSW-NSSFYRLRPELRRAERSKTFPTWV 270
 DB 198 ALVKEDPPESVYAKPVNNPRLEWQNPSSWPDSPFLKPFLLKRR-----LI 248
 QY 271 KQLQHHK-----YIHAWGSLRVVQLRAQEEGCGEWSKSPFAMGTPTESRSP 322
 DB 249 LDQWQHVELSDGTSHTITDAVAGKEYIIVAAKDN-DIGTWSMVSVAVHATPTEE----- 303
 QY 323 AENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMVP 362
 DB 304 -PKHLTEVQITET-----TSTST--STWPP 328

RESULT 18

UHHUCN

ciliary neurotrophic factor receptor alpha precursor - human
 N:Alternate names: CNTF receptor
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1992 #sequence__revision 31-Dec-1992 #text_change 09-Jul-2004
 C/Accession: A40854; A56526
 R:Davis, S.; Altmir, T.H.; Valenzuela, D.M.; Wong, V.; Furch, M.E.; Squinto, S.P.; Yanc
 Science 253, 59-63, 1991
 A>Title: The receptor for ciliary neurotrophic factor.
 A:Reference number: A40854; MUID:91289158; PMID:1648265
 A:Accession: A40854
 A:Molecule type: mRNA
 A:Residues: 1-372 <DNA>
 A:Cross-references: UNIPROT:P26992; GB:M73238
 R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Braman, C.I.; McClain,
 Genomics 25, 157-163, 1995
 A>Title: Genomic organization and chromosomal localization of the human and mouse genes
 A:Reference number: A56526; MUID:95293367; PMID:7774913
 A:Accession: A56526
 A:Molecule type: DNA
 A:Residues: 1-346, S', 348-372 <VAL>
 A:Cross-references: GB:L38025; NID:9608654; PIDN:AAA91337.1; PID:9608656
 C:Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinosit
 C:Comment: The CNTF receptor sequence appears to contain several PEST regions.
 C:Genetics:
 A:Gene: GDB:CNTR
 A:Cross-references: GDB:134652; OMIM:118946
 A:Map position: 9p13-9p13
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C:Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinositol
 F:1-20/Domain: signal sequence #status predicted <Sig>
 F:21-372/Product: ciliary neurotrophic factor receptor #status predicted <Mat>
 F:39-31/Domain: immunoglobulin homology <Imm>
 F:116-296/Domain: cytokine receptor homology <CRS>
 F:46-89/Disulfide Bonds: #status predicted
 F:60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 301; DB 1; Length 372;
 Best Local Similarity 29.2%; Pred. No. 2.2e-13;
 Matches 112; Conservative 44; Mismatches 150; Indels 78; Gaps 18;

QY 6 CALLAALAAFGAALAPRCAPQAVARGVLTSLPGDSVTLTCGVEPEDNATVHWLVRK 65

DB 10 CAVLA---AAAAVVYAQRHSPOE--APHVQERLSDVTLPC-GRANMD-AAVTRVN-- 60
 QY 66 AAGSHPSRWAGGRLLRSVOLHDSGNTSCYR--AGRAGVHLLVDVPEEPQLSCFR 123
 DB 61 --GTLADPLDLNGSQLVHGLGLGSHGACCHRDWSHLRHQVLLHVGVPPEPVLSCS 118
 QY 124 KSPLSNVCEW--SPRSTPSLTTRKAVLLVRK---QNSPADPOEPQCYQSQSCQ 177
 DB 119 NTPYKGFYSWHLPTPTTYTNTFNTVHGSIMCEKDA-----LKNRCH 165
 QY 178 LAVPEDSSF-YIVSMCVASSVGSKFSKTQFGCGILODPDPANITVTAVARNPRLSV 236
 DB 166 IRYMLFSTIKYKVSISVSNALGHN-ATATDEFTIVPDDPENVARPSPRRLRV 224
 QY 237 TWQDPHSW-NSSFYRLRPELRRAERSKTFPTWVKDLOHC-----YHDMSGRL 287
 DB 225 TWQTSWPDPSFPLKFLRYR-----LILDQWQHVELSDGTAHTTDAVAGE 275
 QY 288 HVVQLRAQEEFGGESEWSPFAMGTPTESRSPPAENESTPMQALTTNKDDNILLFRD 347
 DB 276 YIIQVAAKN-EIGTWSMVSVAHATPTEE-----PRHLTEAQAEI----- 318
 QY 348 SANATSLPVEFMVP-----EGE 365
 DB 319 ---TSTSTSLAPPTTKICDPGE 339

RESULT 19

I53394

Soluble interleukin-6 receptor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence__revision 02-Jul-1996 #text_change 23-Jul-1999
 C/Accession: I53394
 R:Horluch, S.; Koyanagi, Y.; Zhou, Y.; Miyamoto, H.; Tanaka, Y.; Waki, M.; Matsumoto, A.
 Eur. J. Immunol. 24, 1945-1948, 1994
 A>Title: Soluble interleukin-6 receptors released from T cell or granulocyte/macrophage

A:Reference number: I53394; MUID:94333499; PMID:8056053
 A:Accession: I53394
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-53 <RES>
 A:Cross-references: GB:S72848; NID:9633862; PIDN:AAC60635.1; PID:9633863
 C:Genetics:
 A:Gene: IL6-GR
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C:Keywords: cytokine receptor

Query Match 7.9%; Score 226; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TPWTSRSPPAENESTPMQALTTNKDDNILLFRDSANATSLP 355
 DB 1 TPWTSRSPPAENESTPMQALTTNKDDNILLFRDSANATSLP 43

RESULT 20

A38957

interleukin 12B precursor [validated] - human
 N:Alternate names: cytotoxic lymphocyte maturation factor 40X chain; natural killer cell
 C:Species: Homo sapiens (man)
 C>Date: 18-Aug-1995 #sequence__revision 18-Aug-1995 #text_change 09-Jul-2004
 C/Accession: A38957; B39359; S21688; B36055
 R:Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Diczig, M.; Lowe, L.; Dzialo, R.; Fj
 J. Immunol. 146, 3074-3081, 1991
 A>Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cyt
 A:Reference number: A38957; MUID:91201875; PMID:1673147
 A:Accession: A38957
 A:Molecule type: mRNA
 A:Residues: 1-328 <WOL>


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QY      248  FVLRRELELYRABERSTFTTMVWVXOLHNCVLIHDMWGLSHVYUOLRAOEGEGGSEMS 307
      367  WLTLVDYELRLKPEAEAEWTFIVGQ-QTHYKFKSLNPKFTIYQIHCKPHD-HGSMSEMS 424
Dh
QY      308  PE-----AMGPTWTEGRS-----PEAENE-----V 327
      425  LEKYLQIDPTDPRIKQNVVWIIIVGLVSLILCLVMSTWTLWLYKRYMIAPILRPVPEPKIGI 484
Dh
QY      328  STPMQALITNNKODDNL-----FRDSANATSLPVEFMVPVPPGED-----SKDVAAPHKQ 376
      485  DTHL--LEFGKSEHLLSALGCHGFPTSCBEILLIYEYLEVDESDQQLMPSHDNGHPSKN 542
Dh
QY      377  PLTSSERIKQI-RYLLDGISALRKRETNKSMGSSKEA-----LLENN 420
Dh
      543  AKMIAETDSDSGRSCDSPSL-SEKCKESPAIILSTQTDIRDVQENN 591

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RESULT 23
I45971
Proactin receptor - bovine
C|Species: Bos primigenius taurus (cattle)
C|Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C|Accession: I45971
R|Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A|Title: Molecular cloning of the bovine proactin receptor and distribution of proactin
A|Reference number: I45971, MUID:93246019, PMID:1338725
A|Accession: I45971
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-581 <SC0>
A|Cross-references: UNIPROT:Q28172, GB:L02549, NID:g163617, PIDN:AAA51417.1, PID:g163618
C|Genetic8:
A|Gene: PKLR
A|3f-221/Domain: cytokine receptor homology <CR8>

Query Match	6.0%	Score 171;	DB 2;	Length 561;
Best Local Similarity	25.0%	Pred. No. 0.00041;		
Matches	51;	Conservative	40;	Mismatches 99; Indels 14; Gaps 7;
QY	113	PPEEPOLSCFRKSPISNVVCEWGPRTSLTTKAVLIVRKTONSPDAEDFOEBCOYSQESQ	172	
Db	27	PPEKPKLVKCSPGKEFTFCWMEBPADGGLPTNYTLTVHK---EGETLIHCSPDYKTGG	82	
QY	173	KFSQQLAVPEEDS-SFYIVSMCVASSVSKSKSKTQTFQCGGLQDDPRANITVTVAANP	231	
Db	83	PNSCYFSQDQTSIMKRVITVNAINQWQISSDPLVHTVYIVVEBPANITLTLEKHPD	142	
QY	232	R-MLSTWQDPHSMN--SSEFYRLFEFLRYAERSKFTT--WMVVDLOHNCVHDWASGL	286	
Db	143	RKPLWMIKMSPTMTDVKSGMFIIOYELRLRKPKATDMEHTHTLQGL--LKIPLLYGQ	200	
QY	287	RHVYQLRAQEEFGCGEMSESGPEA	310	
Db	201	KYLVOIRCKPD--HGYSWSEWSPES	222	

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RESULT 24
I49659          glycoprotein 130 - mouse
C|Species: Mus musculus (house mouse)
C|Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C|Accession: I49659; I48370
R|Saito, M.; Yoshida, K.; Hibi, M.; Tega, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A|Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A|Reference number: I48370; MUID:92291532; PMID:1602143
A|Accession: I49659
A|Status: translated from GB/EMBL/DDBJ
A|Molecule type: mRNA
A|Residues: 1-917 <RES>
A|Cross-references: UNIPROT:Q00560; GB:M8336; NID:g193591; PIDN:AAA37723.1; PID:g193592
A|Accession: I48370

```

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1..917 <R2>
A:Cross-references: EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PID:G840817
C:Genetics:
A:Gene: gp130
C:Keywords: glycoprotein
E:114-314/Domain: cytokine receptor homology <CRS>

Query Match	5.9%	Score 167.5	DB 2	Length 917	.
Best Local Similarity	25.0%	Pred. No. 0.0013			
Matches 58	Conservative 48	Mismatches 89	Indels 37	Gaps 12	

[illegible]

RESULT 25
A36337
membrane glycoprotein gpi30 precursor - human

C:Date: 12-Apr1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C:Accession: A36337
R:Hb1, M.: Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844; PMID:2261637
A:Accession: A36337
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <H1B>
A:Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: Sq11-Sq11
C:Keywords: glycoprotein; membrane protein
C:Keywords: cytokine receptor homology <CRS>
C:Keywords: Domain: cytokine receptor homology <CRS>

Query Match	5.9%	Score 167.5	DB 2	Length 918
Best Local Similarly	22.1%	Pred. No. 0.0013		
Matches 82		Conservative 61	Mismatches 133	Indels 95
				Gaps 19

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QY      106  VHLVADVPEEPQ--LSCCRKSPLSNVCEW--GPRST---PSLTTXAVLLVRFQNSPAD 160
      : : : : : | | | | | : : : : : | | | | | : : : : :
Db      118  ITTISGLPEPRKLNSTLCVNEG--KRCRCMDGRETHETNTLLISEMATHKPAD----- 171
      : : : : : | | | | | : : : : : | | | | | : : : : :
QY      161  FOEPCOYSQESQSCQLAVEBGDSFYIVSMCV---ASSVGSKFSKQTQFOGCGILOP 216
      : : : : : | | | | | : : : : : | | | | | : : : : :
Db      172  ---CKAKRDPT--SCTVDY---STVFVNIEVWVEAENALGKVTSDHINFDPPYKVP 222
      : : : : : | | | | | : : : : : | | | | | : : : : :
QY      217  DPPANITTYTANRPNRLSVTWODPHSNMSYRRLRFELRYAEKSKPTTMMVMD--L 273
      : : : : : | | | | | : : : : : | | | | | : : : : :
Db      223  NPENHLSVINSEELSSILKLTWYNST--KSYLLIKYMIQYTKASTWSQIPEDTAST 280
      : : : : : | | | | | : : : : : | | | | | : : : : :
QY      274  OHHCYIHHAMSGLRHVQDLRAOEERQCEGSEMSWSPDAGTPTPE-----SRSP 324
      : : : : : | | | | | : : : : : | | | | | : : : : :
Db      281  RSLFTVQDLKFTFEVFRIRCKEKEDGKGYMDMSSEAGITVEDRPSKAPSPWYKIDPSH 340
      : : : : : | | | | | : : : : : | | | | | : : : : :
QY      325  NE-----VSTPQA-----LTTNKDD----- 341

```

Db 341 TQGYRTVQLVWKTLPPFENAGKILDYEVLTTRKSHLQNYATNATLTLNLNDRYLATL 400
 Qy 342 ---NIFRISANTSLPV-EFMVPPGDSKDYAAPRPL-----TSSERIDKQIRYL 392
 Db 401 TNRNLVSKSDAVALTLTTPADCFQATHFVMDLK--APFKDNLMLVWETTPRESVYK--YIL 455
 Qy 393 DGISALRKETC 403
 Db 456 EMCVLSDKAPC 466

RESULT 26

A44257
 Interleukin-6 signal transducing molecule gp130 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A44257
 R/Wang, Y.; Neelbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A/Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
 A/Reference number: A44257; MUID:93052397; PMID:1427893
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-918 <MAN>
 A/Cross-references: UNIPROT:P40190
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBI:P118480)
 C/Keywords: transmembrane protein
 F,134-315/Domain: cytokine receptor homology <CRS>

Query Match 5.8%; Score 166; DB 2; Length 918;
 Best Local Similarity 20.2%; Pred. No. 0.0017;
 Matches 99; Conservative 71; Mismatches 171; Indels 150; Gaps 22;
 Qy 106 VHLIVDVPREP-QLSCFRKSPLSNVVCEWGP-RST---PSLTTKAVLVRKFNQNSAED 160
 Db 118 ITILISGVPDPIPTMLSCIVNEG-KQMLCQLDPGRETYLETNYTLKSSWATEKEPD----- 171
 Qy 161 FOEPCQYQSOSQKFSQCLAVEGDSFPIVSMCV---ASSVGSKEFKTQTFQCGGILQP 216
 Db 172 ---CRTHGHTS--SCMM---GYTPYFVNIWVWEAENALGNVSEPIINFDPVDKVP 221
 Qy 217 DPPANITVTAVARPMILSVTWDPHSMNSFTRLRFLRYARBRKSTFTTMVKLOH- 275
 Db 222 SPNHLSTVNSEBLSILKILAM--VNSGLDSILRLKSDIQY---RTKDASTWIQVPLEDT 276
 Qy 276 ---HCVIHDAMSGLRHVVLQRAOEFQGGSEMSPEAMGTPTTE--SRSP----- 321
 Db 277 VSPRTSFTVQDLKPFTEYVFRINSIKENKGWSDMSEASGTTIEDRPSKAFSFWYKN 336
 Qy 322 ---PAE-----NEVSTPMQALTTNKD----- 340
 Db 337 ANHDOETRSARLWKTLPLSEANGKILDYEVLTQSKSVQTYVANGTELIIVLITNRRYV 396
 Qy 341 ---DNILFRDSANATSLP-VFMPVPVPGEDSKDYA-----APHRQPLTSSERID 385
 Db 397 ASLAARVAVGKSPATVLTITGSHFKASHPVVDLKAPPKDNLWVETPPSKVPN----- 450
 Qy 386 KQIRYILIDGISARKETCNKSNMCESSKEALAEENLILPRMAEKQCFQSGFNEETCLVK 445
 Db 451 ---KYL-----EWG-----VLSNSPCIPDMQOEDGTVAR-----TH 480
 Qy 446 IITGLFEFYLYEYLQNRFSSEQARAVQMSKYLQGLQKAKKULDIATTPDPTNAS 505
 Db 481 LRSLLESKCYLTLTPVPVFGGSGPESM-----KAYLKQAPSKGPTVWTK 527
 Qy 506 LLTKLQAOQW 516
 Db 528 KYGKNEAVLEW 538

RESULT 27

A30304
 prolactin receptor 2 precursor - rabbit
 M/Alternate names: prolactin receptor, mammary gland
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: A30304; A60380
 R/Bedery, M.; Jolicoeur, C.; Levi-Meynais, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A/Title: Identification and sequence analysis of a second form of prolactin receptor by n
 A/Reference number: A30304; MUID:89184578; PMID:2289321
 A/Accession: A30304
 A/Molecule type: mRNA
 A/Residues: 1-616 <EDE>
 A/Cross-references: UNIPROT:P14787; GB:J04510; NID:J615669; PIDD:AAA31457.1; PID:J615670
 R/Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A/Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
 A/Reference number: A60380; MUID:91146782; PMID:2289615
 A/Accession: A60380
 A/Molecule type: protein
 A/Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108,150-164,'XX',167-
 A/Note: the amino end of the mature protein was blocked
 C/Keywords: blocked amino end; glycoprotein; transmembrane protein
 F,1-24/Domain: signal sequence #status predicted <SIG>
 F,25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F,36-221/Domain: cytokine receptor homology <CRS>
 F,225-258/Domain: transmembrane #status predicted <TM>
 F,59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 161.5; DB 2; Length 616;
 Best Local Similarity 21.8%; Pred. No. 0.002;
 Matches 71; Conservative 42; Mismatches 141; Indels 71; Gaps 11;
 Qy 113 PREEPQLSCFRKSPLSNVVCEWGPSTPSLTTKAVLVRKFNQNSAEDFOEPCQYQSQ 172
 Db 27 PGKPFIFKCRSPKEKFTPCWWRPGADGCLPTNYLTGHNK-----EGETITHECDYKTKG 82
 Qy 173 KFSQCLAVEGDS-SFYVSMCVASVGSKFSKQTQFGCGGILQBDPPANITVTAVARNP 231
 Db 83 PMSCTFSKSHSITVITITVATNQGSVSDPYVDVTVIVBDDPVLNLTLEVKHPED 142
 Qy 232 R--WLSVTWDPH--SNNSFYRLRFLRYARBRKSTFTTMVKLOHHCYIHDAMSGLR 287
 Db 143 RKPVLWVKMLPPTLVDVNSGULTQYELRLKPKRAEHTHFAQ-QTQFILSLYFGQK 201
 Qy 268 HVOURLAEDEFGQGSMSWSPDA-----M 311
 Db 202 YLVQVRCKPD--HGFWSVSPSSSIQIPNDFTMKDITVWIFVAVLSTICLIWMAVALK 259
 Qy 312 GTPWTSRSPPAENEVSTP-----MQALTTNKDDNIL-----FRDSANATSLPVEFM 359
 Db 260 GYSWVTCIFPP-----VGPCKIKGPDTHLLEKGSBELLSAFGCODFPPTADCDLVEFL 315
 Qy 360 PVPFGE-----SKDYAAPRQP 377
 Db 316 EVDSSEDDQLMPAHSKSHSGPMKP 340

RESULT 28

A29884
 prolactin receptor precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C/Accession: A29884
 R/Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shirota, M.; Banville, Cell 53, 69-77, 1988
 A/Title: Cloning and expression of the rat prolactin receptor, a member of the growth hor
 A/Reference number: A29884; MUID:8815059; PMID:2832068
 A/Accession: A29884
 A/Molecule type: mRNA
 A/Residues: 1-310 <BOU>
 A/Cross-references: UNIPROT:P05710; GB:J419304; NID:9206364; PIDD:AAA41937.1; PID:9206365


```

A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A:Reference number: 157699; MUID:89261824; PMID:2725531
A:Accession: 177524
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-303 <RES>
A:Cross-references: UNIPROT:Q08501; GB:M22958; NID:g200479; PIDN:AAA39976.1; PID:g200480
F:31-216/Domain: cytokine receptor homology <CR>

Query Match      5.4%; Score 155; DB 2; Length 303;
Best Local Similarity 22.6%; Pred. No. 0.0022;
Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

Oy      113 PPEPQLSCFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPQEPQCSQESQ 172
      ||:::|
Db      22 PPGKPEIHKCKSPDKETFTTCWNPQSDGGLPTNYSL-----TYSKEGE 64
Oy      173 K-PSCQLAVDEGDS-----FYVSCVAVSVGSKPKQTQFGCGIILPDP 218
      ||:::|
Db      65 KNYTECDPYKTSGNSCFSGKQYTSIMKTYIIITNATNMGSSITSDPLYDYTVIPEP 124
Oy      219 PANIT--VTAAARNPRMLSVTMDP--HSNNSFYLRLFELRYAERSKTFITMMVLDLQ 274
      ||:::|
Db      125 PRNITLVEYKQKDKKTYLVWVKMLPITITDVTGFTMEYELRLSEEA---DEMEIHFTG 181
Oy      275 HHC--VIHDAMSGLRHVVLPAQEEFGQGEWSEWSEPE 309
      ||:::|
Db      182 HQTFKVFDFYGGQKYLVTQCKPD--HGVSRWGQE 216

RESULT 36
153269
P:prolactin receptor, long form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I53269; J06771; S34356
R:Clarke, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
A:Reference number: I53269; MUID:93307149; PMID:8319571
A:Accession: I53269
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-608 <RES>
A:Cross-references: UNIPROT:Q08501; GB:L14811; NID:g293769; PIDN:AAA02686.1; PID:g293770
R:Moore, R.C.; Oka, T.
Gene 134, 263-265, 1993
A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
A:Reference number: J06771; MUID:94085788; PMID:8262385
A:Accession: J06771
A:Molecule type: mRNA
A:Residues: 1-608 <MOO>
A:Cross-references: GB:LJ3593; NID:g347398; PIDN:AAC37641.1; PID:g347842
R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
Submitted to the EMBL Data Library, June 1993
A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
A:Reference number: S34356
A:Accession: S34356
A:Molecule type: mRNA
A:Residues: 1-557, 'F', 559-608 <EDE>
A:Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
C:Comment: Prolactin receptor have long form and short form which are resulted from alternate splicing. This long form receptor is capable of transducing a signal to milk protein gene.
C:Keywords: receptor; transmembrane protein
F:31-216/Domain: cytokine receptor homology <CR>
F:230-253/Domain: transmembrane #status Predicted &ltTM>

Query Match      5.4%; Score 155; DB 2; Length 608;
Best Local Similarity 22.6%; Pred. No. 0.0056;
Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

Oy      113 PPEPQLSCFRKSPLSNVVCEWGRSTPSLTTKAVLVLRKQNSPADPQEPQCSQESQ 172
      ||:::|

```

Db 22 PGGRPEIKRCSRSPDKETFTCMWNPGRSDGLPTNYSL-----TYSKEGE 64

Oy 173 K--FSCQLAVEBGDS-----FYIYMCVASSVGSKFSTQTFQGGCGLIOPDP 218

Db 65 KNTTECPDPYKTSNGSPSCFSPSKOYTSIMWKYIITVATNATNMSSGTSPLVYDVITYIEPEP 124

Oy 219 PANTT--VTAARARNRMISVTVQDP--HSWNSGFYRLRELRARBARSKFTTMMVMDLQ 274

Db 125 PRNLTEVKQLKDKKTYLAWKKLPPTIIDYKGTGMFWMEIRLKSBEA---DEMEIHFTG 181

Oy 275 HHC--VIHDAMSGLRHVYQLRAQEEFGQGESEMSWPE 309

Db 182 HQTEFKVFDLYPGQKYLVTGRCKPD--HGYSRWMGGE 216

RESULT 37

A53743

N,Alternate names: protein-tyrosine kinase (EC 2.7.1.112) tyros3 precursor - human

C,Species: Homo sapiens (man)

C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #extc_change 09-Jul-2004

C,Accession: A53743; JP00077; J02145; S32765; S32219

R,Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.

J, Biol. Chem. 269, 10720-10728, 1994

A,Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is expressed

A,Reference number: A53743; MUID:94193774; PMID:7511603

A,Accession: A53743

A,Status: preliminary

A,Molecule type: mRNA

A,Residues: 1-890 <MAR>

A,Cross-references: UNIPROT:006418; GB:U05682; NID:9463469; PIDN:AAA19236.1; PID:9463470

R,Onash, K.; Mizuno, K.; Kuma, K.; Miyata, T.; Nakamura, T.

Oncogene 9, 699-705, 1994

A,Title: Cloning of the cDNA for a novel receptor tyrosine kinase, Sky, predominantly exp

A,Reference number: JP0077; MUID:94150991; PMID:8108112

A,Accession: JP0077

A,Molecule type: mRNA

A,Residues: 1-890 <OHA>

A,Cross-references: DDBJ:D17517; NID:9624880; PIDN:BA04467.1; PID:9624881

A,Experimental source: hepatoma HepG2 cell

R,Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Guida, L.C.; B

Gene 134, 289-293, 1993

A,Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.

A,Reference number: J02145; MUID:94085793; PMID:8262388

A,Accession: J02145

A,Molecule type: mRNA

A,Residues: 519-790 <POL>

A,Cross-references: EMBL:X72886; NID:9296020; PIDN:CAA51396.1; PID:g312336

R,Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Altitalo, K.

submitted to the EMBL Data Library, March 1993

A,Description: Human Tyro3 gene and pseudogene in chromosome 15pter-q25.

A,Reference number: S32219

A,Accession: S32765

A,Status: preliminary

A,Molecule type: mRNA

A,Residues: 519-790 <PO2>

A,Cross-references: EMBL:X72886; NID:9296020; PIDN:CAA51396.1; PID:g312336

C,Genetics:

A,Gene: GDB:TYRO3

A,Cross-references: GDB:134764; OMIM:600341

A,Map position: 15q15.1-15q21.1

C,Superfamily: protein-tyrosine kinase axl, fibronectin type III repeat homology; immunog

C,Keywords: ATP; brain; glycoprotein; growth factor receptor; phosphotransferase; transfe

F,1-11/Domain: (or 7-11) signal sequence #status predicted <Sig>

F,42-890/Product: protein-tyrosine kinase tyros3 #status predicted <MAT>

F,60-118/Domain: immunoglobulin homology <IMW>

F,156-205/Domain: immunoglobulin homology <IMW2>

F,322-309/Domain: fibronectin type III repeat homology <FN3A>

F,322-405/Domain: fibronectin type III repeat homology <FN3B>

F,429-451/Domain: transmembrane #status predicted <TM>

F,516-793/Domain: protein kinase homology <KIN>

F,524-532/Region: protein kinase ATP-binding motif

F,63,191,230,240,293,366,380/Binding site: catbolydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 146; DB 1; Length 890;
 Best Local Similarity 23.1%; Pred. No. 0.039; Indels 128; Gaps 18;
 Matches 83; Conservative 30; Mismatches 119;

QY 9 LALLIAPGALAPRCPOAEVARGV---LTSIPGDSVLTCPGVEPEDNATVHV--- 61
 DB 23 LGLLIALASLILPEBAAGLKLKMGAPVLTGSGQGPVLTNC-SYEGMEEPDIOGWKOGA 81
 QY 62 -----LRRKPAAGSHPSRWAGMGRLLRSVOLHSGNYSCT-----RAGRPA----- 103
 DB 82 VQGNLDQLYIPVSEQH---WIGF---LSLKSVERSDAGRWCCVEDGETEISQPVWLT 135
 QY 104 -GYVHLLVD-----VPEEP-QLSCFRKSPLSNVVCEW-----GPRSTPSLTTKAVL 148
 DB 136 EGVPTFVEPRDLAVPRNAPFQLSCENAVGPEPVITVMWGTTIKIGPAPSPSLAVTGV 195
 QY 149 LVRRKQNSPADPQEPQOYSGQSCQQLAVPEGDSFFIVSMCVASVSGSKFTQTF 208
 DB 196 -----TQSTMFSCAHNLKGLAS-----SRTATV 219
 QY 209 QGCGILQ--DPPANITVTAVARNRMLSVTV-----QDPHSMNSSP 248
 DB 220 H-----LQALPAPAFITVTKLSSSN--ASVAMMGADGRALLQSCVQVTAQAGW---- 269
 QY 249 YRLRFELRYRARSKTFTTMMVKDLQHNCHVIDAMSGLRHVQLRAQEFQGGEMSEMS 308
 DB 270 -----EVLAVVVPVPPFT-----CLLRDLVPAVNTSLRVCANALGPSPADWVP 314

RESULT 38

Down syndrome cell adhesion protein 1 - human (fragment)
 N:Alternate names: Down syndrome cell adhesion molecule
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T08851
 R/Yamakawa, K.; Huo, Y. K.; Haendel, M. A.; Hubert, R.; Chen, X. N.; Lyons, G. E.; Korenberg
 submitted to the EMBL Data Library, September 1997
 A:Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down sy
 A:Reference number: Z16495
 A:Accession: T08851
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1896 <YAM>
 A:Cross-references: EMBL:AF023449; NID:G3169765; PID:G3169766
 A:Experimental source: brain; developmental stage: 14 weeks; fetal
 C:Genetics:
 A:Gene: DSCAM
 A:Map position: 21q22
 A>Note: derived from alternately-spliced mRNA
 C:Function:
 A:Description: involved in nervous system development
 C:Keywords: alternative splicing

Query Match 5.0%; Score 144; DB 2; Length 1896;
 Best Local Similarity 23.8%; Pred. No. 0.15; Indels 58; Gaps 15;
 Matches 81; Conservative 49; Mismatches 153;

QY 24 RCPAQOVA-RGVLTSLPGDSVLTTCPGVEPEDNATVHWLRKPAAGSHPSRWAGMGR-- 80
 DB 1269 KAPARILTFSGVTVTTPMKKIDVLPCKAV-GDPSPAVVPM--KDSNGT-PSLVITIDGRKSI 1324
 QY 81 -----LLRSVOLHSGNYSCT-----RAGRPAQVHLLVAVPPEPRQLSCFRKSPLSNVVC 132
 DB 1325 FSNQSFITRTVKAEDSGYISCLANNNGSDEIILNLOQVPPDQPRILT-VSKTSSSITL 1383
 QY 133 EMGPRSTPSLTTKAVLVKRFQV-----SPAEDPQECQYSGSQSOK-----FSCQLA 179
 DB 1384 SWLPDNGGSSIRGYILQYSEDNBSQWSPFIPSEB-----STRLKLTCKGTYKXTLT 1438
 QY 180 VEGGSSFTYVSMCVASVGS--KPSKQTFQCGGILQDPDPANITVTAVARNRMLSVT 237

DB 1439 AONGVGRGISIELIETKLGKEPQFSKEQLF-----ASINTTRVLN-----LIG 1484

QY 238 WDPHSMNSSPFRLRLRELATYRARESKTFTTMMVKDLQHNCHVIDAMSGLRHVQLRAQEE 297
 DB 1485 WNDGGCPRTS-----FTLLYRPPGTTVWTTAORTSLSKSYLIYDLOEATWELQWRVNS 1539

QY 298 FGGGEMSEMEPEAMGTPWTESRSPPAENSVSTPMQALTNK 338
 DB 1540 AG---CAEKQANPATLNTYGSTTTPPLIKSVQNEBGLTNE 1577

RESULT 39

B59405
 prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: B59405; B49400
 R/Hu, Z. Z.; Meng, J.; Dufau, M. L.
 J. Biol. Chem. 276, 41086-41094, 2001
 A:Title: Isolation and characterization of two novel forms of the human prolactin recept
 A:Reference number: A59405; MUID:21538812; PMID:11518703
 A:Accession: B59405
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <HUI>
 A:Cross-references: UNIPROT:Q96P36; GB:AF214012; PIDN:AF214012.1
 R/Hu, Z. Z.
 submitted to GenBank, December, 1999
 A:Reference number: A49400
 A:Accession: B49400
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <HU2>
 A:Cross-references: GB:AF214012; PIDN:AF214012.1
 C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor g
 ta-casien gene promoter activation, with S1b more effective than S1a. However, their lig
 C:Genetics:
 A:Gene: GDB:PRLR
 A:Cross-references: GDB:120315; OMIM:176761
 A:Map position: 5p13.3-5p13.1
 A:Keywords: glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
 F:36-221/Domain: cytokine receptor homology <CRS>
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.8%; Score 138; DB 2; Length 288;
 Best Local Similarity 22.1%; Pred. No. 0.031; Indels 52; Gaps 8;
 Matches 49; Conservative 32; Mismatches 89;

QY 112 VPEEPQLSCFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPADPQEPQOYSGDS 171
 DB 26 LPPEKPEIFKCRSPNKETFTCMWRPDTDGLPTNYSLTVHR-----EGET 70
 QY 172 QKFSQQLAVPEGDS-----FYVSMCVASVSGSKRKTQTFQCGGILQDPDP 219
 DB 71 LMHCRCPIYITGGPWSCHFGKQYTSMMRTYIMVNATNQSSFSDELVDYVTIYQPDPP 130
 QY 220 ANITVTAVARNR--WLSVTWQDPH--SWNSFYRLRFELRYRARESKTFTTMMV----- 270
 DB 131 LELAVEYKQPEDRKPYLMIKSPPTLIDKTGMFTLLYELRLPEKA---AEWEIHFAQ 187
 QY 271 -----KDLOHCHVIDAMSGLRHVQLRAQEEFGGEMSEMS 308
 DB 188 QTEFKILSLH-----FGQKYLQVRCXD--HGYSWAMSP 220

RESULT 40

A59405
 prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: A59405; A49400

R;Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A; Title: Isolation and characterization of two novel forms of the human prolactin receptor
A; Reference number: A59405; MUID:21538812; PMID:11518703

A;Reference number: A59405; MUID:21538812; PMID:11518703

A;Accession: A59405

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-376 <HU1>

A; Cross-references: UNIPROT:Q96P35; GB:AF214012; PIDN:AF214012.1

R;Hu, Z.Z.

submitted to GenBank, December, 1999

A;Reference number: A49400

A;Accession: A49400

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-376 <H02>

A;Cross-references: GB:
C:Comment: This is one

eta-casein gene promoter activation with Slc

ected COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. However, their

C:Genetics:
 ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. Hence

A:Gene: GDB:PRR
c/gene/cb:

A: Cross-reference

A:Map position: 5p13.3-5p13.1

Keywords: glycoprotein; transmembrane protein

```
F;1-24/Domain: signal sequence #status predicted
```

F:25-376/Product: prolactin receptor, short form Sla #

F:36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Abn) (covalent) #status predicted

Query Match 4.8%; Score 138; DB 2; Length 376;

Best Local Similarity 22.1%; Pred. No. 0.044;

Matches 49; Conservative 32; Mismatches 89; Indels 52; Gaps 8;

140 *****

112 VPPEPQLSCFRKSPLSNVCEWGPSTPSLTKAVLLVRKFQNSPAEDFQEPQYSQES 171

[illegible]

D6 26 LPPGKPEIFKCRSPNKETFTCMWRPGTDGGLPTNYSLYTHR-----EGET 70

09 173 OKFSCOI AVEBCDSS-----EYIVSMCUASCVCSKFESKYTOTBOCCGIIADPDB 316

1/2 QKFSCLAVPEGDS-----FYIVSMCVASSVGSKFIQIFGGCGLQDPDP 215

Db 71 I M H E C P D Y T T G S P N S C H E K O V T S M R P T Y I M M V N A T N O M G S S E S D E I Y V D Y T Y I V O P D P 130

DB / 1 LTMHCPDIIIGPNSCHFGKQIISMWRITIMMVNAINQMGSSFSDELIVDVITIVQDPDF 130

220 ANITVTAVARNPB--WLSVTWODPH--SWNSSFYRLBEELRYBRAERSKTFTTMY----- 270

220 ADVI I V I A V A N F N - - W D S V I W Q D F H - - S M N S S I V A N T E D N I A N S N I F I I N N V - - - - - 2 /

Db 131 LELAVEVKOPEDRKPYLWIKWSPPTLIDIKTGWFTLLYEIRLKEPA---AEWEIHFAQO 187

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:40:41 ; Search time 249.038 Seconds

(without alignments)
1254.542 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861
Sequence: 1 MVAVCALLALALAPGAL.....LILRSFKERLQSLRALRQM 543

Scoring cable: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1918	67.0	468	1	IL6A_HUMAN
2	1468	51.3	467	1	IL6A_PIG
3	991	34.6	462	1	IL6A_RAT
4	954.5	33.4	460	1	IL6A_MOUSE
5	938.5	32.8	212	1	IL6_HUMAN
6	938.5	32.8	212	2	AA807539
7	938.5	32.8	212	2	CAG29292
8	907.5	31.7	212	1	IL6_MACFA
9	899.5	31.4	212	1	IL6_MACMU
10	898.5	31.4	209	2	O97540
11	895.5	31.3	212	1	IL6_CERRO
12	801.5	28.0	212	2	O8MKH0
13	799.5	27.9	209	2	O9THH3
14	617.5	21.6	175	2	O9THH4
15	577	20.2	207	2	O9MYZ7
16	574.5	20.1	209	1	IL6_PHOVI
17	571.5	20.0	208	1	IL6_HORSE
18	571	20.0	205	1	IL6_ORCOR
19	562	19.6	208	2	O9XT80
20	561	19.6	207	1	IL6_CANPA
21	558	19.5	211	1	IL6_LAMGL
22	558	19.5	211	2	O865W7
23	557.5	19.5	212	1	IL6_PIG
24	555.5	19.4	212	2	O8MKJ75
25	544.5	19.0	208	1	IL6_FELCA
26	539.5	18.9	160	2	O97535
27	516.5	18.1	207	2	O28403
28	501.5	17.5	214	2	O8MKES
29	482.5	16.9	191	2	O6QHY3
30	482.5	16.9	191	2	AA873282
31	472	16.5	208	1	IL6_CAPHI

32	471	16.5	208	1	IL6_BOVIN	P26892 bos taurus
33	467	16.3	208	1	IL6_SHEEP	P29455 ovine aries
34	466	16.3	208	2	O6V919	O6V919 bubalus bub
35	466	16.3	208	2	AA054301	AA054301 bubalus b
36	437.5	15.3	207	1	IL6_MARMO	O35736 marmota mon
37	435.5	15.2	207	2	O6JHH3	O6JHH3 marmota mon
38	403.5	14.1	528	2	O6UANS	O6UANS tetraodon n
39	403.5	14.1	528	2	AA825684	AA825684 tetraodon n
40	396.5	13.9	211	1	IL6_RAT	P20607 rattus norv
41	382	13.4	241	2	O9MZRI	O9MZRI oryctolagus
42	378	13.2	212	2	O91ZL3	O91ZL3 sigmodon hl
43	374.5	13.1	211	1	IL6_MOUSE	P08505 mus musculu
44	371	13.0	210	2	O9WV08	O9WV08 mesocricetu
45	355	12.4	241	2	O90Y10	O90Y10 gallus gall

ALIGNMENTS

RESULT 1
ID IL6A_HUMAN STANDARD; PRT; 468 AA.
AC P08887; Q16202;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=IL6R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=8305347; PubMed=316546;
RA Yamaoka K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA Taniguchi T., Hirano T., Kishimoto T.;
RA "Molecular structure of interleukin 6 receptor."
RT Proc. Jpn. Acad. B, Phys. Biol. Sci. 64:209-211(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91336983; PubMed=1872801;
RA Schooltink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,
RA Kishimoto T., Heinrich P.C., Rose-John S.;
RA "Structural and functional studies on the human hepatic interleukin-6
RT receptor. Molecular cloning and overexpression in HepG2 cells."
RL Biochem. J. 277:659-664(1991).
RN [4]
RP SEQUENCE OF 313-365 FROM N.A. (ISOFORM 2).
RX MEDLINE=9433499; PubMed=8056053;
RA Horlrich S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
RA Matsumoto A., Yamamoto M., Yamamoto N.;
RA "Soluble interleukin-6 receptors released from T cell or
RT granulocyte/macrophage cell lines and human peripheral blood
RT mononuclear cells are generated through an alternative splicing
RT mechanism."
RL Eur. J. Immunol. 24:1945-1948(1994).
RN [5]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=99167486; PubMed=10066782;
RA Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,
RA Moritz R.L., Simpson R.V.;
RA "Disulfide bond structure and N-glycosylation sites of the
RT extracellular domain of the human interleukin-6 receptor."
RL J. Biol. Chem. 274:7207-7215(1999).

FT STRAND 34 37
 FT TURN 39 40

Query Match 67.0%; Score 1918; DB 1; Length 468;
 Best Local Similarity 96.5%; Pred. No. 1,1e-126;
 Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAFGAALAPRCPAEOVAVGVLTSLPDSYVTLTCPGVEPDNATVHW 60
 DB 1 MLAVGALLAALAAFGAALAPRCPAEOVAVGVLTSLPDSYVTLTCPGVEPDNATVHW 60
 QY 61 VLAKPAAGSHPSWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQVHLVDPVEEPQLS 120
 DB 61 VLAKPAAGSHPSWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQVHLVDPVEEPQLS 120
 QY 121 CFAKSLSNVVCWGRSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFCQLAV 180
 DB 121 CFAKSLSNVVCWGRSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRLSTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRLSTWOD 240
 QY 241 PHSWNSFYRLRRLRYRERSKFTTMMVKDLOHCVIHANSGLRHVVQLRAOEFGQ 300
 DB 241 PHSWNSFYRLRRLRYRERSKFTTMMVKDLOHCVIHANSGLRHVVQLRAOEFGQ 300
 QY 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360
 DB 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360
 QY 361 VPGEEDSKVAP 373
 DB 357 ----QDSSVPLP 365

RESULT 2
 IL6A_PIG STANDARD; PRT; 467 AA.
 AC 018766;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
 GN Name=IL6R;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morris K.R., Strom A.D.G.;
 RT "Cloning and expression of biologically active porcine IL-6 receptor
 alpha chain.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE=Liver;
 RA Klier J.V., Mattern R.L.;
 RT "Partial cDNA sequence of porcine interleukin 6 receptor.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
 with low affinity, but does not transduce a signal. Signal
 activation necessitate an association with IL6ST. Activation may
 lead to the regulation of the immune response, acute-phase
 reactions and hematopoiesis.
 CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (by
 similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in liver.
 CC -1- DOMAIN: The two fibronectin type III-like domains contained in the
 C-terminal part form together a cytokine-binding domain.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein

CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 3.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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DR EMBL: AF147881; AAF73109.1; -;
 DR EMBL: AF015116; AAB70916.1; -;
 DR HSSP: P08887; IN26.
 DR InterPro: IPR002996; Cytokn recept_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003530; Hemptrecept_L_F3.
 DR InterPro: IPR007110; Ig-like.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR PROSITE: PS50853; FN3; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR GlycoProtein: 1
 FT CHAIN 1 19
 FT DOMAIN 20 467
 FT TRANSMEM 365 386
 FT DOMAIN 387 467
 FT DOMAIN 20 112
 FT SITE 303 307
 FT DISULFID 25 193
 FT DISULFID 47 96
 FT DISULFID 121 132
 FT DISULFID 165 176
 FT CARBOHYD 55 55
 FT CARBOHYD 93 93
 FT CARBOHYD 221 221
 FT CARBOHYD 350 350
 SQ SEQUENCE 467 AA; 51066 MM; A2B0B884EF21C502 CRC64;

Query Match 51.3%; Score 1468; DB 1; Length 467;
 Best Local Similarity 75.1%; Pred. No. 5.7e-95;
 Matches 280; Conservative 27; Mismatches 58; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAFGAALAPRCPAEOVAVGVLTSLPDSYVTLTCPGVEPDNATVHW 60
 DB 1 MLAVGALLAALAAFGAALAPRCPAEOVAVGVLTSLPDSYVTLTCPGVEPDNATVHW 60
 QY 61 VLAKPAAGSHPSWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQVHLVDPVEEPQLS 120
 DB 61 VLAKPAAGSHPSWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQVHLVDPVEEPQLS 120
 QY 121 CFAKSLSNVVCWGRSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFCQLAV 180
 DB 121 CFAKSLSNVVCWGRSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSGESQKFCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRLSTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRLSTWOD 240
 QY 241 PHSWNSFYRLRRLRYRERSKFTTMMVKDLOHCVIHANSGLRHVVQLRAOEFGQ 300
 DB 241 PHSWNSFYRLRRLRYRERSKFTTMMVKDLOHCVIHANSGLRHVVQLRAOEFGQ 300
 QY 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360
 DB 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTTNKDDNITLFRDSANATSLPYEFMP 360

Fri Dec 10 08:14:24 2004

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Db      301 GLWSEWSEVGTGIPWTESSRSFATETELPLSTQAPTNEDEDISKESANATSLPV----- 356
QY      361 VPPGEDSKDYAAP 373
          |||
Db      357 -----QDSASVPLP 365

RESULT 3
ID      IL6A_RAT      STANDARD;      PRT;      462 AA.
AC      P22273;
DT      01-AUG-1991 (Rel. 19, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN      Name=Il6r;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Fischer 344; TISSUE=Liver;
RC      MEDLINE=91060602; Pubmed=2174054;
RA      Baumann M., Baumann H., Fey G.H.;
RT      "Molecular cloning, characterization and functional expression of the
RT      rat liver interleukin 6 receptor."
RL      J. Biol. Chem. 265:19853-19862(1990).
RN      [2]
RP      IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA      Gibson T.;
RL      Unpublished observations (FEB-1995).
CC      -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC      with low affinity, but does not transduce a signal. Signal
CC      activation necessitate an association with IL6ST. Activation may
CC      lead to the regulation of the immune response, acute-phase
CC      reactions and hematopoiesis.
CC      -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- DOMAIN: The two fibronectin type III-like domains contained in the
CC      C-terminal part form together a cytokine-binding domain.
CC      -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC      folding and thereby efficient intracellular transport and cell-
CC      surface receptor binding.
CC      -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC      Subfamily 3.
CC      -1- SIMILARITY: Contains 1 fibronectin type III domain.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: MS5857; AAA41431.1; -
DR      PIR: A37986; A37986.
DR      HSSP: P08887; 1N26.
DR      RGD: 2902; 116r.
DR      InterPro: IPR002996; Cytokn_recept_B/G.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR008957; FN_III-like.
DR      InterPro: IPR003530; HemptreceptL_F3.
DR      InterPro: IPR007110; I9-like.
DR      Pfam: PF00041; fn3; 1.
DR      Pfam: PF00047; I9; 1.
DR      PROSITE: PS00853; FN3; 1.
DR      PROSITE: PS01354; HEMATOPO_RBC_L_F3; 1.
DR      PROSITE: PS00835; IG_LIKE; 1.
DR      GlycoProtein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
KW

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FT      SIGNAL      1      19
FT      CHAIN      20      462
FT      DOMAIN      20      364
FT      TRANSMEM      365      365
FT      DOMAIN      366      462
FT      DOMAIN      386      462
FT      DOMAIN      404      408
FT      DOMAIN      404      408
FT      SITE      300      304
FT      SITE      25      190
FT      DISULFID      47      92
FT      DISULFID      117      128
FT      DISULFID      162      173
FT      CARBOHYD      32      32
FT      CARBOHYD      55      55
FT      CARBOHYD      85      85
FT      CARBOHYD      150      150
FT      CONFLICT      227      261
FT      Ref. 1).
SQ      SEQUENCE      462 AA; 50398 MW; A4D6064CEDC0537D CRC64;
Query Match      34.6%; Score 991; DB 1; Length 462;
Best Local Similarity 52.9%; Pred. No. 2.3e-61;
Matches 194; Conservative 51; Mismatches 112; Indels 10; Gaps 6;
QY      1      MLAVGCLALALIAAPAAALARRCPAEOVARGVLTSLPGDVTLLTCGVPEPDNATVHW 60
          |||||
Db      1      MLAVGCLTVALLAAPVALVIGSCRALEVANGVITSLPGAATVLLICGKKAAGNATVHW 60
QY      61      VLKRPAGSHPSRWAGGRLLRLRSVQLHDSGNTSCYARAGPAGVHLVDPPEBPOLS 120
          |||||
Db      61      VY----SGSQRRETTTNGTLVRAVQVNDTGHYLCFLDHLVGVPLLVVPPPEPTLS 116
QY      121      CFRKSPISNVTCENGPRSTPSLTFAVILVRKFPNSPAE-DFOEPCVQSOKRSCOLA 179
          |||||
Db      121      CFRKSPILVACCEHMPSTPSPTTKAMFAKINTNGKSDPQVPCQYSQULKSCEVE 176
QY      117      VREGDSSFFIYVMCVASSVGSKFKTQTFQCGGILQDPDPANITVAVARNPRLSVTWQ 239
          |||||
Db      117      ILEGDKVHIVLCAVANSVGRSHNVFOSLAKVQDPDPAALVSAIPGXPRMLKVSQV 236
QY      180      VREGDSSFFIYVMCVASSVGSKFKTQTFQCGGILQDPDPANITVAVARNPRLSVTWQ 239
          |||||
Db      177      ILEGDKVHIVLCAVANSVGRSHNVFOSLAKVQDPDPAALVSAIPGXPRMLKVSQV 236
QY      240      DPHSNSSYRRLREFLRYAERSKFTTWWKVDLOHHCYHDMASGLRHVYQVRAQEEBG 299
          |||||
Db      237      DPHSNSSYRRLREFLRYAERSKFTTWWKVDLOHHCYHDMASGLRHVYQVRAQEEBG 296
QY      237      DPHSNSSYRRLREFLRYAERSKFTTWWKVDLOHHCYHDMASGLRHVYQVRAQEEBG 296
          |||||
Db      300      QGEWSEWSEVGTGIPWTESSRSFATETELPLSTQAPTNEDEDISKESANATSLPV 356
          |||||
Db      297      ICGWSKMSPEVTGTPMLAERITTPA-GIPGNPTQVSVEDYDNHEDYGSSSTEATSVLAPV 355
          |||||
QY      357      E-FMPVP 362
          |||||
Db      356      QGSSPTP 362
          |||||

RESULT 4
ID      IL6A_MOUSE      STANDARD;      PRT;      460 AA.
AC      P22272;
DT      01-AUG-1991 (Rel. 19, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN      Name=Il6ra; Synonyms=Il6r;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALE/c; TISSUE=Spleen;
RC      MEDLINE=90278354; Pubmed=2112585;
RA      Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,

```


RA Kishimoto T.;
 RT "Functional murine interleukin 6 receptor with the intracellular A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis.";
 RL J. Exp. Med. 171:2001-2009(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Liver;
 RA Fiorillo M.T., Cliberto G., Dente L.;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
 CC with low affinity, but does not transduce a signal. Signal
 CC activation necessitates an association with IL6ST. Activation may
 CC lead to the regulation of the immune response, acute-phase
 CC reactions and hematopoiesis.
 CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: The two fibronectin type III-like domains contained in the
 CC C-terminal part form together a cytokine-binding domain.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 3.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 CC EMBL; X51975; CAA36237.1; -;
 CC EMBL; X53802; CAA37810.1; -;
 CC PIR; J10144; J10144.
 CC PIR; J10145; J10145.
 CC HSSP; P08887; IN26.
 CC MGD; MG1:105304; 116za.
 CC DR InterPro: IPR002996; Cytokn recept_B/G.
 CC DR InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR008957; FN_III-like.
 CC DR InterPro: IPR003530; HemptreceptL_F3.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR Pfam; PF00041; fn3; 1.
 CC DR PROSITE; PS50853; FN3; 1.
 CC DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
 CC DR PROSITE; PS50855; IG_LIKE; 1.
 CC KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 460
 CC FT DOMAIN 20 364
 CC FT TRANSMEM 365 385
 CC FT DOMAIN 386 460
 CC FT DOMAIN 20 116
 CC FT DOMAIN 213 308
 CC FT DOMAIN 404 408
 CC FT SITE 300 304
 CC FT DISULFID 25 190
 CC FT DISULFID 47 92
 CC FT DISULFID 117 128
 CC FT DISULFID 162 173
 CC FT CARBOHYD 32 32
 CC FT CARBOHYD 55 55
 CC FT CARBOHYD 150 150
 CC FT CONFLICT 374 374
 CC SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;
 Query Match 33.4%; Score 954.5; DB 1; Length 460;

Best Local Similarity 50.1%; Pred. No. 8, 5e-59;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;
 QY 1 MAVGCALLAALLAAGALARRCPQAEVAVGLTSLPGDSVTYLTCPGVPEPDNATVFM 60
 DB 1 MLTVGCTLLVALLAAVAVALVIGSCRALEAVANGVTSLGATVTLCPGKAAGNTVTH 60
 QY 61 VLRKPAAGSPRSMAGGRLLRSVQLHDSGVSCYRAGRPAQVTHLLVDVPEEPOLS 120
 DB 61 VY-----SSQKREMTTGTTLVLRDVLSDTGDYLCSDHDLVGTVPPLVDVPEEPKLS 116
 QY 121 CFFKSPSLNVNCEWGRSPSTLTAKVLLVRKFNQSPAR-DPQEPQSQESQKFSQOLA 179
 DB 117 CFFKSNPLVNAICEMRRSPSPPTTAKVLPAAKINTNGKSDFPQVQSQQLKFSQVYE 176
 QY 180 VEBGDSFFIVSMCAVSSVGSFKSTQTPQGGCIILOPPDPANITVAVANRWLSVTWQ 239
 DB 177 ILEGDRVYHIVSLCVANSVSKSSHNEAFHSLKMQDPDPANILVSAIPGRPMLEVSQ 236
 QY 240 DPHSNMSSPYRLRPELRYAERSKPTTMMVVDLOHCVIHDAMSGLRHYVOLAQEBFG 239
 DB 237 HPEITWPSYLLQFQRLRPVMSKETVLLPVAQIQVYIHDLRGVKAVOVGRKEBLD 236
 QY 300 QGEWSEMSPEAMGTPW-TESRSPPEANEVSTPWQALTTNKDDNILFRSANVTSLPVER 358
 DB 297 LGQWSEMSPEVGTGPIAPRTPA-GILMPTQVSEDSANHEDEYESTATSV----- 351
 QY 359 MPVPGEEDSKVDVAAP 373
 DB 352 --LAPVQESSMSLP 364

RESULT 5
 IL6_HUMAN STANDARD; PRT; 212 AA.
 ID IL6_HUMAN
 AC P05231; Q9UCU2; Q9UCU3; Q9UCU4;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
 DE (interferon beta-2) (Hybridoma growth factor) (CTL differentiation
 DE factor) (CDF).
 GN Name=IL6; Synonyms=IFNB2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87065033; PubMed=3491332;
 RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
 RA Kashiyama S.-I., Nakajima K., Koyama K., Iwamatsu A., Tanasawa S.,
 RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
 RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=88082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 RA Nakai S., Kishimoto T.;
 RT "Structure and expression of human B cell stimulatory factor-2 (BSF-
 RT 2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.;
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [4]

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"Structure and expression of cDNA and genes for human interferon-beta-
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Brakenhoff J.P.J., de Groot E.R., Pannekoek H.,
Aarden L.A.;
"Molecular cloning and expression of hybridoma growth factor in
Escherichia coli.";
J. Immunol. 139:4116-4121(1987).
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Tonouchi N., Miwa K., Katsuyama H., Matsui H.;
"Deletion of 3' untranslated region of human Bsp-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3
cells.";
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SEQUENCE FROM N.A.
TISSUE=Fibroblast;
MEDLINE=87004683; PubMed=3758081; Derynck R., Tavernier J.,
Haegeman G., Content J., Voiclaert G., Derynck R., Tavernier J.,
Fiers W.;
"Structural analysis of the sequence coding for an inducible 26-kDa
protein in human fibroblasts.";
Eur. J. Biochem. 159:625-632(1986).
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SEQUENCE FROM N.A.
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"Interleukin 6: identification as a hematopoietic colony-stimulating
factor.";
Mitt. 83:40-47(1988).
[9]
SEQUENCE FROM N.A.
MEDLINE=93178270; PubMed=1291290; Chen Q.Y.;
"Stable and efficient expression of human interleukin-6 cDNA in
mammalian cells after gene transfer.";
Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
[10]
SEQUENCE FROM N.A., AND VARIANTS SER-32 AND VAL-162.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
Nickerson D.A.;
"SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
Submitted (JUN-2001) to the EMBL/GenBank/DBS databases.
[11]
SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straube R.J., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Diatchenko L., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
Stapleton M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
Boesk S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalón D.K., Muzny D.M., Scdegren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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and mouse cDNA sequences.";
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Billiau A.;
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factor activity: IL-1 beta and hybridoma growth factor (HGF).
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SEQUENCE OF 30-50.
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factor for thymocyte in human leukocyte conditioned medium.";
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"Marked cell-type-specific differences in glycosylation of human
interleukin-6.";
Cytokine 3:204-211(1991).
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SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
MEDLINE=95154344; PubMed=7851440; Breton J., la Flura A., Bertolero F., Orsini G., Valasina B.,
Zillicio R., de Filippis V., Polverino de Laureto P., Fontana A.;
"Structure, stability and biological properties of a N-terminally
truncated form of recombinant human interleukin-6 containing a single
disulfide bond.";
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"Disulfide structures of human interleukin-6 are similar to those of
human granulocyte colony stimulating factor.";
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MUTAGENESIS.
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"Evidence for the importance of a positive charge and an alpha-helical
structure of the C-terminus for biological activity of human IL-6.";
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MEDLINE=96134845; PubMed=8555185; Nishimura C., Mitanabe A., Gonda H., Shimada I., Arata Y.;
"Folding topologies of human interleukin-6 and its mutants as studied
by NMR spectroscopy.";
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Cumming D.A.;
"Solution structure of recombinant human interleukin-6.";
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"1.9-A crystal structure of interleukin 6: implications for a novel
mode of receptor dimerization and signaling.";
EMBO J. 16:989-997(1997).
-1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and


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Db      22 LPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYLIDGISAARKETCKNSMNCSS 81
Qy      413 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLNQRFSSSEQAR 472
Db      82 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLNQRFSSSEQAR 141
Qy      473 AVOMSTKVLIOFLQKAKNLDATTPDPPTNASILITKLOAQONWLODMTTHILRSFKEF 532
Db      142 AVOMSTKVLIOFLQKAKNLDATTPDPPTNASILITKLOAQONWLODMTTHILRSFKEF 201
Qy      533 LOSSIRALROM 543
Db      202 LOSSIRALROM 212

RESULT 8
ID IL6_MACPA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name:IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
OX [1]
RN SEQUENCE FROM N.A.
RA Tatsumi M.;
RT "Molecular cloning and expression of cynomolgus monkey interleukin-6."
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
CC EMBL, AB000554; BAA19148.1; -.
CC HSSP, P05231; IL6.
CC InterPro: IPR009079; 4 helix cytokine.
CC InterPro: IPR003573; IL6_MGF_GCSF.
CC InterPro: IPR003574; Interleukin_6.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6GSGFMGF.
CC PRINTS: PR00434; INTERLEUKIN6.
CC ProDom: PD004356; Interleukin_6; 1.
CC SMART, SM00126; IL6; 1.
CC PROSITE, PS00254; INTERLEUKIN_6; 1.
CC Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT CHAIN 1 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 212 AA; 23654 MW; CF8173FCBF08399 CRC64;
Query Match 31.7%; Score 907.5; DB 1; Length 212;

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Best Local Similarity 94.8%; Pred. No. 6,1e-56;
Matches 181; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy      354 LPVGF-WPVPGEDSKDVAAPHROPLTSSERIDKQIRYLIDGISAARKETCKNSMNCSS 412
Db      22 LPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYLIDGISAARKETCKNSMNCSS 81
Qy      413 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLNQRFSSSEQAR 472
Db      82 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLNQRFSSSEQAR 141
Qy      473 AVOMSTKVLIOFLQKAKNLDATTPDPPTNASILITKLOAQONWLODMTTHILRSFKEF 532
Db      142 AVOMSTKVLIOFLQKAKNLDATTPDPPTNASILITKLOAQONWLODMTTHILRSFKEF 201
Qy      533 LOSSIRALROM 543
Db      202 LOSSIRALROM 212

RESULT 9
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name:IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
OX [1]
RN SEQUENCE FROM N.A.
RA STRAIN=RAC 2;
RC MEDLINE=96003435; PubMed=7561102;
RX Vulliamer F.J., Bear S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."
RT J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
CC EMBL, L26028; AAB99978.1; -.
CC HSSP, P05231; IL6.
CC InterPro: IPR009079; 4 helix cytokine.
CC InterPro: IPR003573; IL6_MGF_GCSF.
CC InterPro: IPR003574; Interleukin_6.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6GSGFMGF.
CC PRINTS: PR00434; INTERLEUKIN6.
CC ProDom: PD004356; Interleukin_6; 1.
CC SMART, SM00126; IL6; 1.
CC PROSITE, PS00254; INTERLEUKIN_6; 1.
CC Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT CHAIN 1 212 Interleukin-6.
FT DISULFID 72 78 By similarity.

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FT DISULFID 101 111 By similarity.
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 212 AA; 23728 MW; 4130DF0CFBCCAD CRC64;

Query Match 31.4%; Score 899.5; DB 1; Length 212;
 Best Local Similarity 93.7%; Pred. No. 2.2e-55;
 Matches 179; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 354 LVEF-MPVPGSDSDVAAPHQPTLSSERIDKQIRYILDGSAKRTCKNSNCCSS 412
 DB 22 LPAAFPAPVLPBGDSKVVAAPHQPLTSSERIDKQIRYILDGSAKRTCKNSNCCSS 81

QY 413 KEALAENNINLPKMAEKDCFCFSGFNEETCLVKIITGLLEFVYLYLQNRFPSSSEOR 472
 DB 82 KEALAENNINLPKMAEKDCFCFSGFNEETCLVKIITGLLEFVYLYLQNRFPSSSEOR 141

QY 473 AVQMSKTVLIQFLQKAKKLDATITPDPPTNASLTKLQAQNMLODMTHLILRSFKE 532
 DB 142 AVQMSKTVLIQFLQKAKKLDATITPDPPTNASLTKLQAQNMLODMTHLILRSFKE 201

QY 533 LOSSLRALROM 543
 DB 202 LOSSLRALROM 212

RESULT 10
 ID 097540 PRELIMINARY; PRT; 209 AA.
 AC 097540;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nancyanae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_Taxid=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Pararoyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey."
 RL Immunogenetics 54:645-653 (2002).
 DR EMBL; AF01510; AB01536.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFNGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR SMART; PS00254; INTERLEUKIN_6; 1.
 FT NON_TER 1 1
 FT NON_TER 209 209
 SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 31.4%; Score 898.5; DB 2; Length 209;
 Best Local Similarity 94.7%; Pred. No. 2.6e-55;
 Matches 178; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 354 LVEF-MPVPGSDSDVAAPHQPTLSSERIDKQIRYILDGSAKRTCKNSNCCSS 412
 DB 22 MPAAFPAPVLPBGDSKVVAAPHQPLTSSERIDKQIRYILDGSAKRTCKNSNCCSS 81

QY 413 KEALAENNINLPKMAEKDCFCFSGFNEETCLVKIITGLLEFVYLYLQNRFPSSSEOR 472
 DB 82 KEALAENNINLPKMAEKDCFCFSGFNEETCLVKIITGLLEFVYLYLQNRFPSSSEOR 141

QY 473 AVQMSKTVLIQFLQKAKKLDATITPDPPTNASLTKLQAQNMLODMTHLILRSFKE 532
 DB 142 AVQMSKTVLIQFLQKAKKLDATITPDPPTNASLTKLQAQNMLODMTHLILRSFKE 201

QY 533 LOSSLRAL 540
 DB 202 LOSSLRAL 209

RESULT 11
 ID IL6_CERTO STANDARD; PRT; 212 AA.
 AC P46650;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Cercopithecus torquatus alyx (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecidae; Cercopithecus.
 OX NCBI_Taxid=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJ;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.B., Chikkala N., Ansaari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates";
 RL J. Immunol. 155:3946-3954 (1995).
 CC FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 DR EMBL; L26032; AAA99972.1; -
 DR HSSP; P05231; IL6U.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFNGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR SMART; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 212
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 73 73
 FT CARBOHYD 172 172
 SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 31.3%; Score 895.5; DB 1; Length 212;
 Best Local Similarity 93.2%; Pred. No. 4.3e-55;

Fri Dec 10 08:14:24 2004

Matches 178; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPPGDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 412
 DB 22 LPAAPFAPVPLGSDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 81
 QY 413 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 472
 DB 82 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 141
 QY 473 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 532
 DB 142 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 201
 QY 533 LOSSLRALROM 543
 DB 202 LOSSLRALROM 212

RESULT 12

Q8MKHD PRELIMINARY; PRT; 212 AA.

AC Q8MKHD; MEDLINE=21972723; PubMed=11976788;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Interleukin-6.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OC NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Herold J.M., Laverge A., Kazanji M.;
 RT "Molecular cloning, characterization, and quantification of squirrel
 monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
 RL Immunogenetics 54:20-29(2002).
 DR EMBL; AF294757; AAK92044.1; -.
 DR HSSP; P05231; IL6.
 DR GO; GO:000576; C:extracellular; IEA.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0005138; P:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6 MGF GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SMART; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 212 AA; 23581 MW; FF22CBFA93245479 CRC64;

Query Match 28.0%; Score 801.5; DB 2; Length 212;

Best Local Similarity 85.3%; Pred. No. 1.8e-48;
 Matches 163; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPPGDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 412
 DB 22 MPAPFAPVPLGSDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 81
 QY 413 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 472
 DB 82 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 141
 QY 473 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 532
 DB 142 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 201
 QY 533 LOSSLRALROM 543
 DB 202 LOSSLRALROM 212

DB 202 LOSSLRALROM 212

RESULT 13

Q9TTH3 PRELIMINARY; PRT; 209 AA.

AC Q9TTH3; MEDLINE=22354194; PubMed=12466897;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 OS Aotus lemurinus (Northern gray-necked night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=43147;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patariyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey.";
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF097323; AAF21298.1; -.
 DR GO; GO:000576; C:extracellular; IEA.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0005138; P:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6 MGF GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR NON TER 1
 FT NON TER 209
 SQ SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match 27.9%; Score 799.5; DB 2; Length 209;

Best Local Similarity 86.2%; Pred. No. 2.4e-48;
 Matches 162; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPPGDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 412
 DB 22 MPAPFAPVPLGSDSKDVAAAPHROPLTSSERIDQIRYILDGISAARKETCNKSNCCSS 81
 QY 413 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 472
 DB 82 KEALAENNMLPKMAEKDGCFOGSGFNEETCLVKIITGLLEFVYLEYLQNRFFESSEQAR 141
 QY 473 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 532
 DB 142 AVQNSTKVLIOFLQKAKNIDATITPDPTNLSILTKQAQONQWLODMTHLILRSPEF 201
 QY 533 LOSSLRAL 540
 DB 202 LOSSLRAL 209
 RESULT 14
 Q9TTH4 PRELIMINARY; PRT; 175 AA.
 AC Q9TTH4; MEDLINE=22354194; PubMed=12466897;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 OS Aotus nigriceps (Black-headed owl monkey).
 OS Aotus nigriceps (Black-headed owl monkey).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX	NCBI_TaxID=571175;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22354194; PubMed=12466897;
RA	Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA	Murillo L.A., Patarroyo M.B.;
RT	"Identification, cloning, and sequencing of different cytokine genes
RT	in four species of owl monkey.";
RL	Immunogenetics 54:645-653(2002).
DR	EMBL: AF097332; AAF21297.1; "-
DR	GO: GO:0005576; C:extracellular; IEA.
DR	GO: GO:0005125; F:cytokine activity; IEA.
DR	GO: GO:0005118; F:Interleukin-6 receptor binding; IEA.
DR	GO: GO:0006955; P:Immune response; IEA.
DR	InterPro: IPR003079; 4 helix cytokine.
DR	InterPro: IPR003573; IL6 MGF GCSP.
DR	InterPro: IPR003574; Interleukin_6.
DR	Pfam: PF00489; IL6; 1.
DR	PRINTS: PRO0433; IL6GCSFMGF.
DR	PRINTS: PRO0434; INTERLEUKIN6.
DR	ProDom: PD004356; Interleukin_6; 1.
DR	SMART: SM00126; IL6; 1.
DR	ProSITE: PS00254; INTERLEUKIN_6; 1.
DR	NON TER
QO	SEQUENCE 175 AA; 12905 MW; 2BCCE574C9B9B189 CRC64;

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Query Match      21.6%; Score 617.5; DB 2; Length 175;
Best Local Similarity 81.8%; Pred. No. 1.3e-35;
Matches 124; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

QY      354 LPVEF-MPVPEGDSKVDAAPHROPITSSERRIDKQIRYLIDGISALRKETCNKSMCESS 412
Db      22 MPAAFPAPVPPIGEDSKVEVAADPNRQLTSTEQIDKHRIYILGSIASLRKEIDCKSMCESS 81

QY      413 KEALAENNINLPKPAEKDGCOSGNGNETCLVKIITGLLEFVYIYIYQNFPESEEQAR 472
Db      82 QEALAENNINLPKPAEKDGCOSGNGNETCLKITITGLLEFVYIYIYQNFPESEEQAR 141

QY      473 AVQMSKVLIIQLOKAKNLDIAITPPDP 500
Db      142 AVQMSKGLIOSLOKAKNLSAIRTPDP 169

RESULT 15
Q9MYZ7 PRELIMINARY; PRT; 207 AA.
AC Q9MYZ7
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin-6.
GN Name-IL-6;
OS Carls familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Young H.-Y., Shin I.-S.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF215796; AAF86275.1; -.
DR HSSP; P05231; IL6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_CGSP.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6CGSPMGF.

```

```
DR PRINTS, PR00434, INTERLEUKIN6.
DR ProDom, PD004356, Interleukin_6; 1.
DR SMART, SM00126, IL6; 1.
DR PROSITE, PS00254, INTERLEUKIN_6; 1.
SQ SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;
```

Query Match	20.2%	Score 577	DB 2	Length 207
Best Local Similarity	54.5%	Pred. NO. 1	1e-32	
Matches 116	Conservative 37	Mismatches 54	Indels 6	Gaps 2

OY	331	MOALTITKNDODNIIIFRDSANANTS.PVEFMPVPEPDESDQVAAHPROPTITSEERIDKOARY	390
OY	1	MNSISTSAFSGILGL---WATAPEPT---PGLPADGSDKDDATSNLSPLTSANKYBELIKY	54
OY	391	ILDGISALRKETCNKSNCESSKALAEENNINLPEMAEKDGFOSGFNEETCLVIKITGL	450
OY	55	ILGHSIALRKEMCMCFKPCEDSKALAEENNIAHLKLEGGKOCFOSGFNOETCLRITGL	114
OY	451	LEFEVYLEYIIONRRSESEBOARAVOMSTKVLIOFLQKAKNLDIATPPDPTNNSLTKL	510
OY	115	VEFOLHTIINIIONNNEGKKNKVSVMHSTKITVLWKLKSKVKVQODVETTPDPPTDASLQAIL	174
OY	511	QAONOWIADMTHLILRSFKFELOSSALRQOM	543
OY	175	QSDQEWLGHITTHILIRSLDEDFQFSLPAVIM	207

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RESULT 16
ID_IL6_PHOVI STANDARD; PRT; 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN Name=IL6;
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidaron T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -I FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions. It plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -I SUBCELLULAR LOCATION: Secreted.
CC -I SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; L46802; AAB01430.1; -.
CC HSSP; P05231; IL6.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSP.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSPMGF.
CC PRINTS; PR00434; INTERLEUKIN6.

```

DR Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 KM Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 209 Interleukin-6.
 FT DISULFID 69 75 By similarity.
 FT DISULFID 98 108 By similarity.
 SQ SEQUENCE 209 AA; 23483 MW; 7514922E43B48E9 CRC64;
 Query Match 20.1%; Score 574.5; DB 1; Length 209;
 Best Local Similarity 58.0%; Pred. No. 1.7e-32;
 Matches 112; Conservative 36; Mismatches 42; Indels 3; Gaps 1;
 QY 351 ATSLPVEFMVPVPGEDSKDVAAPHROPLTSERIDKQIRYIIDGIALKRETCNKNCE 410
 DB 20 ATAFPT---PQVGGESQADATSNRPPLTSPDKMEEFIKYILGKISALKNEMCKKNCE 76
 QY 411 SSEKALAEKNLNLPMKAEKDCGFGSGNEETCLVKIITGLLEFEVYLEYQNRFSSEBQ 470
 DB 77 DSKEALAEKNLNLPMKAEKDCGFGSGNEETCLVKIITGLLEFEVYLEYQNRFSSEBQ 136
 QY 471 ARAVQNSTVYLQFLQKAKNLDATTPPTTNASLITKQAOQOMQDMTTHLIIRSPK 530
 DB 137 ANSVYISTKLVLQVLMKAKVKSODEVTTPPTTDSLOAILKQDKMLKHTTHILRSLE 196
 QY 531 EFLQSLRLALROM 543
 DB 197 DFLQSLRLAVRIM 209
 RESULT 17
 IL6_HORSE STANDARD; PRT; 208 AA.
 AC 095181; 019007; 046568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20579380; PubMed=1137120;
 RA Swiderski C.E., Sobol G., Lunn D.P., Horohov D.W.;
 RT "Molecular cloning, sequencing, and expression of equine interleukin-6";
 RT 6"; Immunol. Immunopathol. 77:213-220(2000).
 RL Vet. Immunol. Immunopathol. 77:213-220(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Leutenegger C.M., Huder J.B., von Rechenberg B., Auer J.;
 RT "Molecular cloning of equine interleukin-6";
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Lai A.C.K.;
 RT "Cloning and expression of equine interleukin-6";
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U64794; AAB67703.1; -
 DR EMBL; AF005227; AAB62246.1; -
 DR EMBL; AF041975; AAC04574.1; -
 DR PIR; T09216; T09216.
 DR HSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6CSGFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 KM Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27 Interleukin-6.
 FT CHAIN 28 208 By similarity.
 FT DISULFID 69 75 By similarity.
 FT DISULFID 98 108 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 71 71 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 184 184 Ls -> FF (in Ref. 1).
 FT CONFLICT 4 5 T -> A (in Ref. 3).
 FT CONFLICT 8 8 I -> V (in Ref. 2).
 FT CONFLICT 137 137 V -> I (in Ref. 3).
 FT CONFLICT 205 205
 SQ SEQUENCE 208 AA; 23325 MW; A62P4C234056FP66 CRC64;
 Query Match 20.0%; Score 571.5; DB 1; Length 208;
 Best Local Similarity 58.5%; Pred. No. 2.8e-32;
 Matches 113; Conservative 32; Mismatches 41; Indels 7; Gaps 3;
 QY 351 ATSLPVEFMVPVPGEDSKDVAAPHROPLTSERIDKQIRYIIDGIALKRETCNKNCE 410
 DB 23 ATAFPT---PLPGEDERTSNP---LITADTKQHIIKYLGIKISALKNEMCKKNCE 76
 QY 411 SSEKALAEKNLNLPMKAEKDCGFGSGNEETCLVKIITGLLEFEVYLEYQNRFSSEBQ 470
 DB 77 DSKEALAEKNLNLPMKAEKDCGFGSGNEETCLVKIITGLLEFEVYLEYQNRFSSEBQ 136
 QY 471 ARAVQNSTVYLQFLQKAKNLDATTPPTTNASLITKQAOQOMQDMTTHLIIRSPK 530
 DB 137 IKMQISTKLVLQVLMKAKVKSODEVTTPPTTDSLOAILKQDKMLKHTTHILRSLE 195
 QY 531 EFLQSLRLALROM 543
 DB 196 DFLQSLRLAVRIM 208
 RESULT 18
 IL6_ORCOR STANDARD; PRT; 205 AA.
 AC 028747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6) (Fragment).
 GN Name=IL6;
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 OC NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hami K.D.,
 RA Stott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from

RT the harbor seal (*Phoca vitulina*), killer whale (*Orcinus orca*), and
 RT Southern sea otter (*Enhydra lutris nereis*)."
 RL Immunogenetics 43:190-195 (1996).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L46803; AAB01429.1; -.
 CC HSSP: P05231; 1ALU.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 1
 FT CHAIN 22 21 By similarity.
 FT DISULFID 64 70 Interleukin-6.
 FT DISULFID 93 103 By similarity.
 FT CARBOHYD 164 164 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;
 Query Match 20.0%; Score 571; DB 1; Length 205;
 Best Local Similarity 59.4%; Pred. No. 3e-32;
 Matches 114; Conservative 29; Mismatches 45; Indels 4; Gaps 2;
 QY 351 ATSLPEFMPVPPGSDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSMCE 410
 DB 15 ATAFPT---PGPLGSEDFKDDTTSRLYLISPDKTBALIKYILGKISAMRKEMCEKDKCE 71
 QY 411 SSKKALAEENNLNLPKAEKDGCGFSGFNEBETCLVKITITGLFEFVLEYLQNFESSEQ 470
 DB 72 NSEKALAEENNLNLPKAEKDGCGFSGFNEBETCLVKITITGLFEFVLEYLQNFESSEQ 470
 QY 471 ARAVQSTVLYIQFLQKAKNLDATTPPTTNASILTKLQAKN-OVLQDMTHLILRSF 529
 DB 132 IEAVQISSTKALQILRKQKYNPDVETTPPTTNASIMNVLQSDNDMMKTKIILIRSL 191
 QY 530 KEFLQSLRAIR 541
 DB 192 ENFLQPSLRAIR 203
 RESULT 19
 Q9XT80 PRELIMINARY; PRT; 208 AA.
 AC 09XT80;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 6.
 OS Delphinapterus leucas (Beluga whale).
 OS Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodactyla; Delphinapterus.
 OC NCBI_TaxId=9749;

RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20141864; PubMed=10678396;
 RA St-Laurent G., Archambault D.,
 RT "Molecular cloning, phylogenetic analysis and expression of beluga
 RT whale (*Delphinapterus leucas*) interleukin 6,"
 RL Vet. Immunol. Immunopathol. 73:31-44 (2000).
 DR EMBL: AF076643; AAD42929.1; -.
 DR HSSP: P05231; 1ALU.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; P:cytokine activity; IEA.
 DR GO: GO:0005138; P:interleukin-6 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;
 Query Match 19.6%; Score 562; DB 2; Length 208;
 Best Local Similarity 58.9%; Pred. No. 1.3e-31;
 Matches 113; Conservative 28; Mismatches 47; Indels 4; Gaps 2;
 QY 351 ATSLPEFMPVPPGSDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSMCE 410
 DB 18 ATAFPT---PGPLGSEDFKDDTTSRLYLISPDKTBALIKYILGKISAMRKEMCEKDKCE 74
 QY 411 SSKKALAEENNLNLPKAEKDGCGFSGFNEBETCLVKITITGLFEFVLEYLQNFESSEQ 470
 DB 75 NSEKALAEENNLNLPKAEKDGCGFSGFNEBETCLVKITITGLFEFVLEYLQNFESSEQ 470
 QY 471 ARAVQSTVLYIQFLQKAKNLDATTPPTTNASILTKLQAKN-OVLQDMTHLILRSF 529
 DB 135 IEAVQISSTKALQILRKQKYNPDVETTPPTTNASIMNVLQSDNDMMKTKIILIRSL 194
 QY 530 KEFLQSLRAIR 541
 DB 195 ENFLQPSLRAIR 206
 RESULT 20
 IL6_CANFA STANDARD; PRT; 207 AA.
 ID IL6_CANFA
 AC P41323;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxId=9615;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mongrel;
 RX MEDLINE=94303924; PubMed=7913298;
 RA Kukiela G.L., Youker K.A., Hawkins H.K., Perrard J.L., Michael L.H.,
 RA Ballantyne C.M., Smith C.W., Entman M.L.;
 RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
 RT reperfusion,"
 RL Ann. N. Y. Acad. Sci. 723:258-270 (1994).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U12234; AAA83030.1; --
 CC HSSP: P05231; IL6.
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003573; IL6 MGF GCSF.
 CC InterPro: IPR003574; Interleukin_6.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PRINTS: PR00434; INTERLEUKIN6.
 CC ProDom: PD004356; Interleukin_6; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 CC KW SIGNAL 20
 CC CHAIN 21 207 Interleukin-6.
 CC FT DISULFID 67 73 By similarity.
 CC FT DISULFID 96 106 By similarity.
 CC SEQUENCE 207 AA; 22945 MW; 45540154EA93C0F50 CRC64;
 SQ
 Query Match 19.6%; Score 561; DB 1; Length 207;
 Best Local Similarity 53.5%; Pred. No. 1.5e-31;
 Matches 114; Conservative 38; Mismatches 55; Indels 6; Gaps 2;
 QY 331 MQALTNNKDDNITLFRDSANATSLPVEFMVPPVPGEDSKDVAAPHROPTSSERIDKOIRY 390
 DB 1 MNSISTAFSLGILL--VNATAPPT--PGIAGDSKDDATNSLPLTSANKVELIKY 54
 QY 391 ILDGISALRKETCKNSNMCSSEKALANNLNIPKAEKDCGFGSGFNEETCLVYITGL 450
 DB 55 ILGKISALRKEMCKFKKCEKSEKALANNLNIPKLGKDCGFGSGFNEETCLVITGL 114
 QY 451 LEFEVLEYLONRSESEBOARAVOMSTKYLIOLOKAKANLDAITTPPTNASILTKL 510
 DB 115 VEFQIHNLITLONNYEGDENKSVHMTKILVOMLSKVNQGEVTPPTDASIALTL 174
 QY 511 QAONQWLODMTTHILIRSEKFEIQQSLRALRQM 543
 DB 175 QSQDECVAHTTHILIRSLDEPLQPSLRAVRIM 207
 RESULT 21
 IL6_LAMGL STANDARD; PRT; 211 AA.
 ID IL6_LAMGL
 AC 0865X6;
 DT 23-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OC NCB1_TaxID=9844;
 OX NCB1
 RN SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RT
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).

CC -I- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB107647; BAC75384.1; --
 CC HSSP: P05231; IL6.
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003573; IL6 MGF GCSF.
 CC InterPro: IPR003574; Interleukin_6.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PRINTS: PR00434; INTERLEUKIN6.
 CC ProDom: PD004356; Interleukin_6; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Acute phase; Cytokine; Growth factor; Signal.
 CC KW SIGNAL 29
 CC CHAIN 30 211 Interleukin-6.
 CC FT DISULFID 71 77 By similarity.
 CC FT DISULFID 100 110 By similarity.
 CC SEQUENCE 211 AA; 23988 MW; BB82D263F096B16 CRC64;
 SQ
 Query Match 19.5%; Score 558; DB 1; Length 211;
 Best Local Similarity 56.5%; Pred. No. 2.5e-31;
 Matches 109; Conservative 35; Mismatches 45; Indels 4; Gaps 2;
 QY 351 ATSLPVEFMVPPVPGEDSKDVAAPHROPTSSERIDKOIRYILDGISALRKETCKNSNMCE 410
 DB 23 ATAPPT--PVPLIGDFDQ--GTSKRPTSPDKBELIKILIRISMRKEMCEKDYDCE 78
 QY 411 SKSEKALANNLNIPKAEKDCGFGSGFNEETCLVYITGLLEFEVLEYLONRSESEBO 470
 DB 79 NSKEALANNLNIPKTEKDCGFGSGFNEETCLMRTITGLLEFQIYDLYONRYEGKGN 138
 QY 471 ARAVOMSTKYLIOLOKAKANLDAITTPPTNASILTKLQAONQWLODMTTHILIRSEK 530
 DB 139 TEAVQSTALALQILAKOKAPEEVSVPNPTGSSLLAKLQTEHQMMKNTGMLIRSL 198
 QY 531 EPIQSSLRALRQM 543
 DB 199 DFLOPSLRAVRIM 211
 RESULT 22
 PRELIMINARY; PRT; 211 AA.
 ID 0865W7;
 AC 0865W7;
 DT 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, last annotation update)
 DE Interleukin 6.
 GN Name=IL-6;
 OS Camelus bactrianus (Bactrian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OC NCB1_TaxID=9837;
 OX NCB1
 RN SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RT
 CC EMBL: AB107656; BAC75393.1; --
 CC HSSP: P05231; IL6.
 CC GO: GO:0005576; C:extracellular; IEA.
 CC GO: GO:0005125; F:cytokine activity; IEA.
 CC GO: GO:0005138; F:interleukin-6 receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 211 AA; 23929 MW; 0DF8004A1A16625FE CRC64;
 Query Match 19.5%; Score 558; DB 2; Length 211;
 Best Local Similarity 57.0%; Pred. No. 2.5e-31;
 Matches 110; Conservative 34; Mismatches 45; Indels 4; Gaps 2;

QY 351 ATSLPVEFWPPGSDSKVAAPHROPITSSERIDQRIYLDGIALRKETCNKSMCE 410
 DB 23 ATAFPT--PVLGSEDFKQGTTSNR-PFTSPDKSEELIKYILGRISAMKEMCEKYDCE 78
 QY 411 SSKKALANNLNLPMKAEKDCGFGSGFNEETCLVKITITGLFEVYLLEYLQNRFFESSEQ 470
 DB 79 NSKEALANNLNLPMKAEKDCGFGSGFNEETCLMKRTITGLFEVYLLEYLQNRFFESSEQ 138
 QY 471 ARAVQSTKVLIQFLQKAKNLDATTPPTTNASLITLQKQONQMLQMTHTLIRSK 530
 DB 139 TEAVQISTKALIQFLQKQKQKQPEVSTPNPTITSSILNKLTQENQMKTKMLIRSL 198
 QY 531 EFLQSLRALROM 543
 DB 199 DFLQSLRALRIM 211

RESULT 23

ID IL6_PIG STANDARD; PRT; 212 AA.
 AC P26893; Q95KN6;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91338547; PubMed=1873476;
 RA Richard C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92360284; PubMed=1497880;
 RA Mathias N., Bixby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330(1992).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Meishan; TISSUE=Blood;
 RA Liu S., Meng M., Gao R.;
 RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan
 hybrid swine.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants.
 CC -!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the IL-6 superfamily.

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CC EMBL; M86722; AAC37333.1; -;
 CC EMBL; M80258; AAC27127.1; -;
 CC EMBL; AF309651; AAG27730.1; -;
 CC PIR; I46590; I46590.
 CC PIR; I46621; I46621.
 CC HSSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.
 FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CONFLICT 30 30 E -> G (in Ref. 1).
 SQ SEQUENCE 212 AA; 23952 MW; 1E736FB230B4FC5D CRC64;

Query Match 19.5%; Score 557.5; DB 1; Length 212;
 Best Local Similarity 57.5%; Pred. No. 2.8e-31;
 Matches 111; Conservative 32; Mismatches 47; Indels 3; Gaps 1;

QY 351 ATSLPVEFWPPGSDSKVAAPHROPITSSERIDQRIYLDGIALRKETCNKSMCE 410
 DB 23 ATAFPT--PVLGSEDFKQGTTSNR-PFTSPDKSEELIKYILGRISAMKEMCEKYDCE 79
 QY 411 SSKKALANNLNLPMKAEKDCGFGSGFNEETCLVKITITGLFEVYLLEYLQNRFFESSEQ 470
 DB 80 NSKEALANNLNLPMKAEKDCGFGSGFNEETCLMKRTITGLFEVYLLEYLQNRFFESSEQ 139
 QY 471 ARAVQSTKVLIQFLQKAKNLDATTPPTTNASLITLQKQONQMLQMTHTLIRSK 530
 DB 140 TEAVQISTKALIQFLQKQKQKQPEVSTPNPTITSSILNKLTQENQMKTKMLIRSL 199
 QY 531 EFLQSLRALROM 543
 DB 200 DFLQSLRALRIM 212

RESULT 24

ID O8MJ75 PRELIMINARY; PRT; 212 AA.
 AC O8MJ75;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE IL-6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Lee D., Yoo H., Choi I.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF518322; AAM74938.1; -;
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.

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	CC	-----
	CC	EMBL, I16914; AAA16620.1; -
	DR	EMBL, D13227; BAA02507.1; -
	DR	Pir, I46084; I46084.
	DR	HSPB, P05231; I1166.
	DR	Interpro, IPRO09079; I16 MGf GCSF.
	DR	Interpro, IPRO03573; I16 MGf GCSF.
	DR	Interpro, IPRO03574; Interleukin_6.
	DR	Pfam, PF00489; I16; 1.
	DR	PRINTS: PRO0433; IL6GCSFMFG.
	DR	PRINTS: PD00434; INTERLEUKIN_6.
	DR	Prodrom, PD00435; Interleukin_6; 1.
	DR	SMART, SMO0126; I16; 1.
	KW	PROSITE, PS00254; INTERLEUKIN 6; 1.
	DR	Acute phase; cytokine; Glycoprotein; Growth factor; Signal.
	FT	SIGNAL 1 27 Potential.
	FT	CHAIN 28 208 Interleukin-6.
	FT	DISULFID 68 74 By similarity.
	FT	DISULFID 97 107 T -> N (in Ref. 2).
	FT	CONFELCT 2 2 S -> P (in Ref. 2).
	FT	CONFELCT 45 45 E -> K (in Ref. 2).
	FT	CONFELCT 133 133 AKLOSCEMLRHHTI -> LSCSHRYVAEAHNN (in Ref. 2).
	FT	CONFELCT 173 187 RS -> LR (in Ref. 2).
	SO	SEQUENCE 208 AA; 23401 MW; 93BA45GBE2989CA4C CRC64;
	QY	Query Match 19.0%; Score 544.5; DB 1; Length 208;
	QY	Best Local Similarity 55.4%; Pred. No. 2,2e-30;
	QY	Matches 107; Conservative % 33; Mismatches 46; Indels 7; Gaps 2
	DB	351 ATSLPVEFMPPVPREDSDVAAAPHOPLTSSRIDKQIRYIIIDGISALKRETCKNSMCE 470
	DB	23 AIAFPPT---PGPLGSD---ATSNRRLPIISADRMELIKYIIIGKISALPKEMCNVNYKE 75
	QY	411 SSAEEAENNLM.PMAEKDCGCFOSGNERTCI.VKIITGLAEFEVYLELNPRESESEQ 135
	DB	76 DSKEALAENNLM.PLAEKDCGCFOSGNERTCI.LRTITGLQFOYLKFLDQKVGDEEN 135
	QY	471 ARAYONSTKYLFLOAKKANLD.AITTPDDPTYNASLLTYLQAONOMLODMTHILLSEFK 530
	DB	136 AKSYVTSTNVLOWLKGKKNDDEVTIIPVIVEWGLAQKSQSEWLRRTHILTLRLLE 195
	QY	531 EFLOSSLRALROM 543
	DB	196 DFLOPSLRARVM 208
	RESULT 26	
	O97535	PRELIMINARY; PRT; 160 AA.
	ID O97535	
	AC O97535;	
	DT 01-MAY-1999 (TREMBLrel. 10, Created)	
	DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
	DT 01-MAY-2004 (TREMBLrel. 26, last annotation update)	
	DT Interleukin-6 (Fragment).	
	DE Name=IL-6;	
	GN Acutus vociferans (Spix's owl monkey).	
	OS Acutus vociferans (Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Eukaryota; Metazoa; Chordata; Platyrrhini; Cebidae; Actinae; Actus.	
	OC Mammalia; Eutheria; Primates; plathyrrini; Cebidae; Actinae; Actus.	
	OX NCBI_TaxID=57176;	
	RN [1]	
	RP SEQUENCE FROM N.A.	
	RX MEDLINE=22354194; PubMed=12466897;	
	RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,	
	RA Murillo L.A., Patatroyo M.B.;	
	RT "Identification, cloning, and sequencing of different cytokine genes	
	RT in four species of owl monkey.";	

RL Immunogenetics 54:645-653 (2002).
 DR EMBL: AF014505; AAD01531.1; -
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR NON_TER 1 1
 FT SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;
 Query Match 18.9%; Score 539.5; DB 2; Length 160;
 Best Local Similarity 84.3%; Pred. No. 3,5e-30;
 Matches 107; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 354 LPVPEFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
 DB 22 MPAAFPAPVPLGSDSKVAAPNQLITSTEQIDKHIRYILEGIALRKETICDKSNMCESS 81
 QY 413 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSSSEQ 472
 DB 82 KEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSSSEQ 141
 QY 473 AVQMSK 479
 DB 142 AVQMSK 148
 RESULT 27
 Q28403 PRELIMINARY; PRT; 207 AA.
 AC Q28403;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 6 (Fragment).
 GN Name=IL-6;
 OS Euhadra lutris (Sea otter).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
 OC Euhadra.
 OC NCBI_TaxID=34882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9613018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Scott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Euhadra lutris nereis).";
 RL Immunogenetics 43:190-195 (1996).
 DR EMBL: L46804; AAB01428.1; -
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 FT NON_TER 1 1

SQ SEQUENCE 207 AA; 23527 MW; 729E0CD91136D8B CRC64;
 Query Match 18.1%; Score 516.5; DB 2; Length 207;
 Best Local Similarity 53.9%; Pred. No. 2.1e-28;
 Matches 104; Conservative 37; Mismatches 47; Indels 5; Gaps 2;
 QY 351 ATSLPVEFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 410
 DB 20 ATAPFT---PGPLGSGSDKDATSNRPPLTSADKMEPFKILGKISALRNEMCDKYNKE 76
 QY 411 SSKEALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSSSEQ 470
 DB 77 DSKEVALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSSSEQ 136
 QY 471 ARAVQMSKVLQFLQKAKNDATITPDPTNASILTLQONOMLOMTTHLILRSFK 530
 DB 137 AHSVYISTHLLQTL--RPNQILEVTPPTDASLQALFKSDQKWLKHTHLILRLR 194
 QY 531 EFLQSSLRALRQW 543
 DB 195 DFLQPSLRALRIM 207
 RESULT 28
 Q8MKES PRELIMINARY; PRT; 214 AA.
 AC Q8MKES;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wu M., Gao R., Li J., Meng M., Long Z., Tang M., Liu S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF493992; AAM27192.1; -
 DR HSP: P05231; IALU.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 214 AA; 23765 MW; 50849FB04D0BDD7F CRC64;

Query Match 17.5%; Score 501.5; DB 2; Length 214;
 Best Local Similarity 57.3%; Pred. No. 2.5e-27;
 Matches 98; Conservative 28; Mismatches 36; Indels 9; Gaps 2;
 QY 351 ATSLPVEFMPVPG---EDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSN 407
 DB 23 ATAPFT-----DRLBEDKGDATSDKMLTSPDTEELIKYILGKISAMRKMECKYE 76
 QY 408 MCSSEKALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSS 467
 DB 77 KENSKEVALAENNINLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFFSS 136
 QY 468 BEQARAQVQSTKVLQFLQKAKNDATITPDPTNASILTLQONOMLOMTTHLILRSFK 518
 DB 137 KGNVEAVQISTKALITLQKQKGNPDKATTPNPTNAGLGLDKLQSONEMWK 187

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RESULT 29
Q6QHY3 PRELIMINARY; PRT; 191 AA.
ID Q6QHY3
AC Q6QHY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Interleukin-6 (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien R., Berger S., Griffin F.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY540191; AAS73282.1; -
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON TER 1 191
SQ SEQUENCE 191 AA; 21677 MW; 5936607DB4D3C1A0 CRC64;

Query Match 16.9%; Score 482.5; DB 2; Length 191;
Best Local Similarity 49.7%; Pred. No. 4.6e-26;
Matches 95; Conservative 40; Mismatches 49; Indels 7; Gaps 3;

QY 349 ANATSLVEFMPVPEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSNM 408
DB 8 AMASAFPT---PGLGEDFRKNDTPPSRLILTPPKTEALIKHIVDKISMRKEICEKNDK 64
QY 409 CESSKKALENNINLPRMAEKDGCFOGFGNEETCLVKITITGLLEFEVYLEYONRPFSSSE 468
DB 65 CENSKETLAENNINLPRMKEKDCFOGFGNETCLIRSTVGLLEYQYLDYLQNEYEGDQ 124
QY 469 EQRNAVQMSKVLQLOKAKRDLATTPPTNASTLTLOQONOMLODMTHLILRS 528
DB 125 ENVKDLRSSIRTLQIMRQ--KSIDLVT--ATTNPDLERKQSSNEWNAKIILILRS 180
QY 529 FKEFLQSSLR 539
DB 181 LENFLQPSLR 191

RESULT 30
AAS73282 PRELIMINARY; PRT; 191 AA.
ID AAS73282
AC AAS73282;
DT 29-MAR-2004 (TREMBLrel. 27, Created)
DT 29-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 29-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Interleukin-6 (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien R., Berger S., Griffin F.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY540191; AAS73282.1; -
FT NON TER 1 191

```

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FT NON TER 191 191
SQ SEQUENCE 191 AA; 21677 MW; 5936607DB4D3C1A0 CRC64;

Query Match 16.9%; Score 482.5; DB 2; Length 191;
Best Local Similarity 49.7%; Pred. No. 4.6e-26;
Matches 95; Conservative 40; Mismatches 49; Indels 7; Gaps 3;

QY 349 ANATSLVEFMPVPEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCKNSNM 408
DB 8 AMASAFPT---PGLGEDFRKNDTPPSRLILTPPKTEALIKHIVDKISMRKEICEKNDK 64
QY 409 CESSKKALENNINLPRMAEKDGCFOGFGNEETCLVKITITGLLEFEVYLEYONRPFSSSE 468
DB 65 CENSKETLAENNINLPRMKEKDCFOGFGNETCLIRSTVGLLEYQYLDYLQNEYEGDQ 124
QY 469 EQRNAVQMSKVLQLOKAKRDLATTPPTNASTLTLOQONOMLODMTHLILRS 528
DB 125 ENVKDLRSSIRTLQIMRQ--KSIDLVT--ATTNPDLERKQSSNEWNAKIILILRS 180
QY 529 FKEFLQSSLR 539
DB 181 LENFLQPSLR 191

RESULT 31
IL6_CAPHI STANDARD; PRT; 208 AA.
ID IL6_CAPHI
AC Q283319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; PubMed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
cells.";
RL Int. Arch. Allergy Immunol. 113:409-416 (1997).
CC -I- FUNCTION: It plays a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
DR EMBL; D86569; BAA1318.1; -.
DR HSSP; P05231; IL6.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.

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FT SIGNAL 1 29 By similarity.
FT CHAIN 30 208 Interleukin-6.
FT DISUFID 72 78 By similarity.
FT DISUFID 101 111 By similarity.
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 16.5%; Score 472; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 2.9e-25;
Matches 93; Conservative 34; Mismatches 51; Indels 4; Gaps 2;

QY 360 PVPGEKSDKVAAPHROPTSSERIDKQIRYLIDGISAARKETCNKNMCESSKEALAEV 419
DB PGLGEDFNDTTPSRLTLTPTEKTEALIKRWDKISARKKEICEKNDECSKETLAEN 88
QY 420 NNTLPMAEKDCGFGSGFNEETLVKIIITGLLEFEVYLEYLQNRPFSSSEQARAVGMSTK 479
DB KKLTPMEERKDCGFGSGFNOAICLRITTAGLEQYLYDLQNEYEGNEVARDLRKNIR 148
QY 480 VLIQFLQKAKNLDATITPDPTTNASLITKLOAQNOMLODMTHLILRSFKEPLQSSLR 539
DB 149 TLIQILKEKAGL--ITT--PATNTDMLERKQSSNEWVGNAKYIILIRLENFLQPSLR 204
QY 540 LR 541
DB 205 IR 206

RESULT 32
IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26B92;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RA MEDLINE=93076003; PubMed=1446077;
RA Droogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
RA "Nucleotide sequence of bovine interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; X57317; CAA40572.1; -.
CC PIR; A56610; A56610.
CC HSSP; P05231; IL6.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.

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DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 208 Interleukin-6.
FT DISUFID 72 78 By similarity.
FT DISUFID 101 111 By similarity.
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 208 AA; 23758 MW; A0F00B9BA2EC341 CRC64;

Query Match 16.5%; Score 471; DB 1; Length 208;
Best Local Similarity 51.6%; Pred. No. 3.4e-25;
Matches 94; Conservative 33; Mismatches 51; Indels 4; Gaps 2;

QY 360 PVPGEKSDKVAAPHROPTSSERIDKQIRYLIDGISAARKETCNKNMCESSKEALAEV 419
DB PGLGEDFNDTTPGGLTLTPTEKTEALIKRWDKISARKKEICEKNDECSKETLAEN 88
QY 420 NNTLPMAEKDCGFGSGFNEETLVKIIITGLLEFEVYLEYLQNRPFSSSEQARAVGMSTK 479
DB KKLTPMEERKDCGFGSGFNOAICLRITTAGLEQYLYDLQNEYEGNEVARDLRKNIR 148
QY 480 VLIQFLQKAKNLDATITPDPTTNASLITKLOAQNOMLODMTHLILRSFKEPLQSSLR 539
DB 149 TLIQIL--KQKTADLITT--PATNTDMLERKQSSNEWVGNAKYIILIRLENFLQPSLR 204
QY 540 LR 541
DB 205 IR 206

RESULT 33
IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E., Barcham G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RA "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA.";
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Borahim B.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC -----
 CC EMBL; X62501; CAA44363.1; -
 DR EMBL; X68723; CAA48662.1; -
 DR EMBL; A19159; CAA01443.1; -
 DR PIR; S29549; S29549.
 DR HSP; P05231; I16.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; I16_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; I16; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PRODOM; P0004356; Interleukin_6; 1.
 DR SMART; SM00126; I16; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Growth factor; Signal.
 KM SIGNAL 1 29 By similarity.
 FT CHAIN 1 29 Interleukin-6.
 FT DISULFID 30 208 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CARBOHYD 38 38 N-linked (GLCNAC. . .) (Potential).
 FT CONFLICT 4 4 I -> R (in Ref. 2).
 FT CONFLICT 110 110 I -> V (in Ref. 2).
 FT CONFLICT 171 171 M -> L (in Ref. 2).
 FT CONFLICT 201 201 S -> R (in Ref. 2).
 SQ SEQUENCE 208 AA; 23446 MW; EEC996C1B3230A0 CRC64;

Query Match 16.3%; Score 467; DB 1; Length 208;
 Best Local Similarity 50.5%; Pred. No. 6.4e-25;
 Matches 92; Conservative 35; Mismatches 51; Indels 4; Gaps 2;

QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGFLGDFPKNDTPGRLLITTPKTEALIKRWVDKISARKETCEKNDECSSKOTLAEN 88
 QY 420 NLNLPKMAEKDCQSGFNEETCIYKITTGLFEVYLEYLONFESSSEQAQAVOMSTK 479
 DB 89 KNLKPKMEKDCQSGFNOAICLIRTAGLEVOYIDYLONEGRENREVDLRKNIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOAQONQLODMTHLILRSKPEFLOSLRA 539
 DB 149 TLIQIL--KQKADITTT--PATNTDLERKQSSNEWKAKITILIRNLNFIQFSIRA 204
 QY 540 LR 541
 DB 205 IR 206

RESULT 34
 O6V919 PRELIMINARY; PRT; 208 AA.

ID O6V919
 AC OCV919;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Interleukin 6.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 OC NCBI_TaxID=89462;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Premraj A., Sreekumar E., Rasool T.J.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY347710; AA054301.1; -
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; I16_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; I16; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.

DR PRODOM; P0004356; Interleukin_6; 1.
 DR SMART; SM00126; I16; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;

Query Match 16.3%; Score 466; DB 2; Length 208;
 Best Local Similarity 51.1%; Pred. No. 7.6e-25;
 Matches 93; Conservative 33; Mismatches 52; Indels 4; Gaps 2;

QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGFLGDFPKNDTPGRLLITTPKTEALIKRWVDKISARKETCEKNDECSSKOTLAEN 88
 QY 420 NLNLPKMAEKDCQSGFNEETCIYKITTGLFEVYLEYLONFESSSEQAQAVOMSTK 479
 DB 89 KNLKPKMEKDCQSGFNOAICLIRTAGLEVOYIDYLONEGRENREVDLRKNIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOAQONQLODMTHLILRSKPEFLOSLRA 539
 DB 149 TLIQIL--KQKADITTT--PATNTDLERKQSSNEWKAKITILIRNLNFIQFSIRA 204
 QY 540 LR 541
 DB 205 IR 206

RESULT 35
 AA054301 PRELIMINARY; PRT; 208 AA.

ID AA054301
 AC AA054301;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Interleukin 6.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 OC NCBI_TaxID=89462;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Premraj A., Sreekumar E., Rasool T.J.;
 RA "Identification and molecular characterization of major Th2 cytokines
 of Indian water buffalo (Bubalus bubalis)."
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY347710; AA054301.1; -
 DR SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;

Query Match 16.3%; Score 466; DB 2; Length 208;
 Best Local Similarity 51.1%; Pred. No. 7.6e-25;
 Matches 93; Conservative 33; Mismatches 52; Indels 4; Gaps 2;

QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGFLGDFPKNDTPGRLLITTPKTEALIKRWVDKISARKETCEKNDECSSKOTLAEN 88
 QY 420 NLNLPKMAEKDCQSGFNEETCIYKITTGLFEVYLEYLONFESSSEQAQAVOMSTK 479
 DB 89 KNLKPKMEKDCQSGFNOAICLIRTAGLEVOYIDYLONEGRENREVDLRKNIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOAQONQLODMTHLILRSKPEFLOSLRA 539
 DB 149 TLIQIL--KQKADITTT--PATNTDLERKQSSNEWKAKITILIRNLNFIQFSIRA 204
 QY 540 LR 541
 DB 205 IR 206

RESULT 36
 IL6_MARMO STANDARD; PRT; 207 AA.
 ID IL6_MARMO
 AC 035736;


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DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN NCBITaxID=9995;
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=98139533; PubMed=9472070;
RA Lohrengel B., Lu M., Roggendorf M.;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6.";
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
DR EMBL; Y14139; CAA74571.1; -.
DR HSSP; P05231; 1ALU.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 1 18 Potential.
FT DISULFID 19 207 Interleukin-6.
FT DISULFID 65 71 By similarity.
FT DISULFID 94 104 By similarity.
SQ SEQUENCE 207 AA; 23770 MW; F30D19F86AD6A600 CRC64;
Query Match 15.3%; Score 437.5; DB 1; Length 207;
Best Local Similarity 45.4%; Pred. No. 7,7e-23;
Matches 88; Conservative 39; Mismatches 62; Indels 5; Gaps 2;
QY 351 ATSLPVEFMPVPGEBSKVAAAPHRQPLTSSERIDKQIRYILGIGSLARKETCNKSMCE 410
DB 16 ATAFPASELQREDGENSVTRNKPTR--ASSGTRRQISYLIRKVEPMRKELECKNDCTCI 72
QY 411 SSKEALAEENLNLPKPAEKDCGFCGSGFNEETCLVKITITGLLEFEVLYEYLNPFESSEEQ 470
DB 73 KSHVAVSENNLPNPKTEKDCGFCGTGYNRDCLVRITSGLEFQVLYIRYIRNKFQEGNNR 132
QY 471 ARA--VQMGSTKVLIOFLQKAKNLDAITPDPPTNASLTKLOAQONQWLQDMTHLILRS 528
DB 133 DRAEHVQSSKALIEILKQEVKDPNKIVPSPPTANINILAKESQNDQWKMTQGLISN 192
QY 529 KFEFLQSSSLRALRQ 542
DB 193 FEDFLQFTLRAVRK 206

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RESULT 37
Q9JHH3 PRELIMINARY; PRT; 207 AA.
AC Q9JHH3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-6.
GN Name=IL-6;
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN NCBITaxID=9995;
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Li D.H., Cullen U.M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Li D.H., Cullen U.M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=21536769; PubMed=11679978;
RA Hodgson P.D., Michalak T.I.;
RT "Augmented hepatic interferon gamma expression and T-cell influx
RT characterize acute hepatitis progressing to recovery and residual
RT lifelong virus persistence in experimental adult woodchuck hepatitis
RT virus infection.";
RL Hepatology 34:1049-1059(2001).
DR EMBL; AF012808; AAF34861.1; -.
DR EMBL; AF12896; AAF28673.1; -.
DR EMBL; AF333966; AAF52717.1; -.
DR HSSP; P05231; 1ALU.
DR GO; GO:0005576; Extracellular; IEA.
DR GO; GO:0005128; F-cytokine activity; IEA.
DR GO; GO:0005138; F-interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 207 AA; 23645 MW; AD2F46E450E13470 CRC64;
Query Match 15.2%; Score 435.5; DB 2; Length 207;
Best Local Similarity 45.4%; Pred. No. 1.1e-22;
Matches 88; Conservative 38; Mismatches 63; Indels 5; Gaps 2;
QY 351 ATSLPVEFMPVPGEBSKVAAAPHRQPLTSSERIDKQIRYILGIGSLARKETCNKSMCE 410
DB 16 ATAFPASELQREDGENSVTRNKPTR--ASSGTRQGISYLIRKVEPMRKELECKNDCTCI 72
QY 411 SSKEALAEENLNLPKPAEKDCGFCGSGFNEETCLVKITITGLLEFEVLYEYLNPFESSEEQ 470
DB 73 KSHVAVSENNLPNPKTEKDCGFCGTGYNRDCLVRITSGLEFQVLYIRYIRNKFQEGNNR 132
QY 471 ARA--VQMGSTKVLIOFLQKAKNLDAITPDPPTNASLTKLOAQONQWLQDMTHLILRS 528
DB 133 DRAEHVQSSKALIEILKQEVKDPNKIVPSPPTANINILAKESQNDQWKMTQGLISN 192
QY 529 KFEFLQSSSLRALRQ 542
DB 193 FEDFLQFTLRAVRK 206

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RESULT 38

or send an email to license@sb-sib.ch).

CC
CC EMBL; M26744; AAA77659.1; -;
DR EMBL; M26745; AAA1430.1; -;
DR PIR; A34247; A34247.
DR HSSP; P05231; IALU.
DR RGD; 2901; IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSE.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 211 Interleukin-6.
FT DISULFID 70 76 By similarity.
FT DISULFID 99 109 By similarity.
SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 13.9%; Score 396.5; DB 1; Length 211;
Best Local Similarity 39.4%; Pred. No. 6, 1e-20;
Matches 76; Conservative 53; Mismatches 59; Indels 5; Gaps 3;

QY 351 ATSLPVEFMPVPPGSDSKVVAAPHROPLTSSERIDKQIRIYLDGISALRKETCKNSMCE 410
DB 22 ATAFPTS--QVRRGDFTEDTT--HNRPVYTTSCVGGITVLRILEMRKELCNGNSDCM 77
QY 411 SSKKALAEENNLNPKMAEKDGFSGSPNEETCLVKIITGLFEFVYLEYQNR-ESSEE 469
DB 78 NSDDALSENNLKLPEIQKNDGCFQIGYNOEICLKICSGLEFRFYLEFVKNLQDKKD 137
QY 470 QARAVQSTKVLIQFLQKAKNLDAITTPDPTNASLTLQAQONQMLQDMTHILRSF 529
DB 138 KARVIGSNTEVLVHIFKQEKDSYKIVLPPTSNALLMEXLESQKELRTKTIQLILKAL 197
QY 530 KEFLQSSLRALRQ 542
DB 198 EEFLKVTMRSTRQ 210

Search completed: December 9, 2004, 09:20:54
Job time : 252.038 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:55:07 ; Search time 1.14568 Seconds
(without alignments)
1091.766 Million cell updates/sec

Title: US-09-462-416-1

Perfect score: 67

Sequence: 1 EFGAGLVLCGQFM 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	68.7	382	2 AC3118	transcription regu
2	46	68.7	402	2 D98169	trcr protein (Arl9
3	46	68.7	1171	1 QOKBFP	pyruvate (flavodox
4	42	62.7	396	2 B75290	hypothetical prote
5	41	61.2	291	2 E71491	probable geranyl t
6	41	61.2	313	2 S66962	probable membrane
7	41	61.2	347	2 D83605	probable binding p
8	41	61.2	623	2 S56206	probable membrane
9	41	61.2	920	2 C70668	probable membrane
10	40	59.7	232	1 S28609	phosphoadenyl-L-su
11	40	59.7	492	2 A87471	hypothetical prote
12	40	59.7	579	2 B82085	sensory box/GGDEF
13	40	59.7	1617	2 B86483	protein F505.15 [l
14	39	58.2	220	2 E71857	probable outer mem
15	39	58.2	230	2 C64658	outer membrane pro
16	39	58.2	274	2 H72521	probable thiazole
17	39	58.2	308	2 H81685	conserved hypotet
18	39	58.2	622	2 B71326	probable V-type AT
19	39	58.2	770	2 S56805	probable RNA helic
20	38.5	57.5	880	2 F83386	hypothetical prote
21	38	56.7	127	2 A53952	profilin - fibron
22	38	56.7	147	2 AG3578	hypothetical prote
23	38	56.7	171	2 T11285	NADH dehydrogenas
24	38	56.7	249	2 T09139	26S proteasome alp
25	38	56.7	249	2 G84667	20S proteasome sub
26	38	56.7	272	2 A84747	hypothetical prote
27	38	56.7	298	2 AD2715	ABC transporter, m
28	38	56.7	348	2 T06385	probable Fe(II) tr
29	38	56.7	389	2 T28954	hypothetical prote

30	38	56.7	390	2 T40924	nuclear localizati
31	38	56.7	494	2 G97496	integral membrane
32	38	56.7	630	2 AB3463	hypothetical membe
33	38	56.7	748	2 G96498	hypothetical prote
34	38	56.7	754	2 AB0614	probable compen
35	38	56.7	1195	2 S76592	5-methyltetrahydro
36	37	55.2	61	2 D64012	hypothetical prote
37	37	55.2	150	2 J50297	infection structur
38	37	55.2	181	2 AH1737	NADH-dependent FMN
39	37	55.2	233	2 A72786	probable transport
40	37	55.2	261	2 AE1471	hypothetical prote
41	37	55.2	303	2 A71529	hypothetical prote
42	37	55.2	352	2 S45558	cytochrome c-type
43	37	55.2	413	2 JC2520	beta-fructofuranos
44	37	55.2	416	2 D84638	probable sarcosine
45	37	55.2	418	2 H83316	isocitrate dehydro

ALIGNMENTS

RESULT 1
AC3118
transcription regulator, ROK family Atu4567 [imported] - Agrobacterium tumefaciens (stra)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #ext_change 09-Jul-2004
C:Accession: AC3118
R:Wood, D.W.; Sebald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Genthner, D.; Kuyavirin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; M0ID:21608550; PMID:11743193
A:Accession: AC3118
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <KUR>
A:Cross-references: UNIPROT:Q8U787; GB:AE008689; PIDN:AA45361.1; PID:gl7743056; GSPDB:G
A:Experimental source: strain C58 (dupont)
C:Genetics:
A:Gene: Atu4567
A:Map position: linear chromosome

Query Match 68.7%; Score 46; DB 2; Length 382;
Best Local Similarity 80.0%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEGAGLVLCGQ 11
DB 226 FEGAGLVLCGQ 235

RESULT 2
trcr protein (Arl96574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 09-Jul-2004
C:Accession: D98169
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Molim, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A:Reference number: A97359; M0ID:21608551; PMID:11743194
A:Accession: D98169
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-402 <KUR>
A:Cross-references: UNIPROT:Q8U787; GB:AE007870; PIDN:AAK88878.1; PID:gl5158645; GSPDB:G
A:Gene: AGR_L_609
A:Map position: linear chromosome

R.Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D. V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66929
A:Accession: S66962
A:Molecule type: DNA
A:Residues: 1-313 <BOH>
A:Cross-references: UNIPROT:Q12067; EMBL:Z74987; NID:g1420238; PID:e251990; PID:g1420239
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:ATX2
A:Cross-references: SGD:S0005605; MIPS:YOR079C
A:Map position: 15R
C:Keywords: transmembrane protein
F:7-23/Domain: transmembrane #status predicted <TM1>
F:76-92/Domain: transmembrane #status predicted <TM2>
F:106-122/Domain: transmembrane #status predicted <TM3>
F:160-176/Domain: transmembrane #status predicted <TM4>
F:184-200/Domain: transmembrane #status predicted <TM5>
F:222-238/Domain: transmembrane #status predicted <TM6>
F:294-310/Domain: transmembrane #status predicted <TM7>

Query Match 61.2%; Score 41; DB 2; Length 313;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQFM 13
DB 73 QFGIGMLGTSFM 85

RESULT 7
D83605
probable binding protein component of ABC transporter PA0323 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83605
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.D.; Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83605
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <STO>
A:Cross-references: UNIPROT:Q916G8; GB:AE004470; GB:AE004091; NID:g9946164; PIDN:AA0371
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0323
C:Superfamily: Escherichia coli spermidine/putrescine-binding protein

Query Match 61.2%; Score 41; DB 2; Length 347;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAAGLVGGQ 11
DB 11 FAAGLALGGQ 20

RESULT 8
S56206
probable membrane protein YFL049w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S56206
R:Murkanti, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasamatsu, T.
submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae
A:Reference number: S56186
A:Accession: S56206
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-623 <MUR>
A:Cross-references: UNIPROT:P43554; EMBL:D50617; NID:g836685; PID:d1009830; PID:g836706;
C:Genetics:
A:Cross-references: SGD:S0001845
A:Map position: 6L
C:Keywords: transmembrane protein
F:121-137/Domain: transmembrane #status predicted <TM1>

Query Match 61.2%; Score 41; DB 2; Length 623;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
DB 194 EFGAGVATGGQ 204

RESULT 9
C70668
probable mmpL7 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70668
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70668
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-920 <COL>
A:Cross-references: UNIPROT:P96289; GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CAB06107.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: mmpL7

Query Match 61.2%; Score 41; DB 2; Length 920;
Best Local Similarity 76.9%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 2 FGAAGLV--GGQF 12
DB 876 FGAAGLVSGGSF 888

RESULT 10
S28609
phosphoadenylyl-sulfate reductase (thioredoxin) (EC 1.8.4.8) - Synechococcus sp. (strain N:Altenate names: 3'-phosphoadenylylsulfate reductase, thioredoxin dependent; PAPS reduced; contains: 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (EC 2.8.2.-)
C:Species: Synechococcus sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S28609
R:Nienhaus, A.; Gisselmann, G.; Schwenn, J.D.
Plant Mol. Biol. 20, 1179-1183, 1992
A:Title: Primary structure of the Synechococcus PCC 7942 PAPS reductase gene.
A:Reference number: S28609; MUID:9309269; PMID:1463852
A:Accession: S28609
A:Molecule type: DNA
A:Residues: 1-232 <NIE>
A:Cross-references: UNIPROT:O55309; EMBL:M84476; NID:g154543; PIDN:AAA27328.1; PID:g15454
C:Genetics:
A:Gene: par
C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase
C:Keywords: cysteine biosynthesis; oxidoreductase; sulfotransferase

Query Match 59.7%; Score 40; DB 1; Length 232;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFAGLVLGGQF 12
|||||
Db 30 EFAGLVLGGTSF 41

RESULT 11
A87471
hypothetical protein CCI789 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87471
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klot
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87499; MUID:21173698; PMID:11259647
A:Accession: A87471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <STO>
A:Cross-references: UNIPROT:Q9A7D4; GB:AE005673; NID:913423219; PIDN:AAK23765.1; GSPDB:G
C:Genetics:
A:Gene: CCI789

Query Match 59.7%; Score 40; DB 2; Length 492;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVLGG 10
|||||
Db 93 FGAGLVLGG 101

RESULT 12
B82085
sensory box/GDEF family protein VC2370 [imported] - Vibrio cholerae (strain N16961 serc
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82085
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charidson, D.; Ermolaeva, M.D.; Vamthekavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 447-453, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82085
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-579 <HEI>
A:Cross-references: UNIPROT:Q9KJ7; GB:AE004307; GB:AE003852; NID:93656934; PIDN:AAF9551
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2370
A:Map position: 1

Query Match 59.7%; Score 40; DB 2; Length 579;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVLGG 10
|||||
Db 13 FGAGLVLGG 21

RESULT 13
B86483
protein FSU5.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86483
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86483
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1617 <STO>
A:Cross-references: UNIPROT:Q9SKV5; GB:AE005172; NID:96598587; PIDN:AAF18642.1; GSPDB:GNC
C:Genetics:
A:Gene: FSU5.15
A:Map position: 1

Query Match 59.7%; Score 40; DB 2; Length 1617;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFAGLVLGGQFM 13
|||||
Db 458 EFAGLVLGGQFM 470

RESULT 14
E71857
probable outer membrane protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71857
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Webberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathc
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <ARN>
A:Cross-references: UNIPROT:Q9ZKA5; GB:AE001531; GB:AE001439; NID:94155617; PIDN:AAD0661;
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1034

Query Match 58.2%; Score 39; DB 2; Length 220;
Best Local Similarity 63.6%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVLGGQFM 13
|||||
Db 70 GAGLVLGGQFM 80

RESULT 15
C64658
outer membrane protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64658
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64658
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-230 <TOM>
 A:Cross-references: UNIPROT:O25735; GB:AE000617; GB:AE000511; NID:G2314256; PIDN:AAD0816
 C:Genetics:
 A:Start codon: GTG

Query Match 58.2%; Score 39; DB 2; Length 230;
 Best Local Similarity 63.6%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGQFM 13
 DB 80 GEGVLGGRFV 90

RESULT 16

H72521
 probable thiazole biosynthetic enzyme ABE2149 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: H72521
 R:Kawababayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; NUID:99310339; PMID:10382966
 A:Accession: H72521

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-274 <RAW>
 A:Cross-references: UNIPROT:Q9Y9Z0; DDBJ:AP000063; NID:G5105654; PIDN:BAAB1160.1; PID:G5

C:Genetics:
 A:Experimental source: strain K1

A:Gene: ABE2149
 C:Superfamily: thiamin biosynthesis protein th1

Query Match 58.2%; Score 39; DB 2; Length 274;
 Best Local Similarity 72.7%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAGLVGQFM 13
 DB 68 GGGLWLGQFM 78

RESULT 17

H81685
 conserved hypothetical protein TC0598 [imported] - Chlamydia muridarum (strain N195)

C:Species: Chlamydia muridarum, Chlamydia trachomatis Mohn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: H81685
 R:Read, T.D.; Brumm, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodeon, R.; Gilm, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mohn and Chlamydia pneumoniae A39.
 A:Reference number: A81500; NUID:20150255; PMID:10684935

A:Accession: H81685
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-308 <TET>

A:Cross-references: UNIPROT:Q9PK72; GB:AE002328; GB:AE002160; NID:G710627; PIDN:AAF3943
 A:Experimental source: strain N195 (Mohn)

C:Genetics:
 A:Gene: TC0598

Query Match 58.2%; Score 39; DB 2; Length 308;
 Best Local Similarity 87.5%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGAGLVG 9
 DB 105 FGAGLVG 112

RESULT 18

B71326
 probable V-type ATPase, subunit I (atp1-1) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: B71326
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rean, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDer
 chey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; NUID:98332770; PMID:9665876
 A:Accession: B71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-622 <COL>
 A:Cross-references: UNIPROT:O83444; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AA66541;

A:Experimental source: strain Nichols
 C:Genetics:

A:Gene: TP0429

Query Match 58.2%; Score 39; DB 2; Length 622;
 Best Local Similarity 53.8%; Pred. No. 88;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGQFM 13
 DB 460 EFGSLMLGQMV 472

RESULT 19

S56805
 probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein J1250; protein YJL033w
 C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S56805; C34848

R:Pohl, T.M.; Aljinovic, G.
 submitted to the Protein Sequence Database, September 1995

A:Reference number: S56793
 A:Accession: S56805

A:Molecule type: DNA
 A:Residues: 1-770 <TOV>

A:Cross-references: UNIPROT:P20448; EMBL:Z49308; NID:G1008154; PIDN:CAA89324.1; PID:G1008

R:Chang, T.H.; Arenas, J.; Abelson, J.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1571-1575, 1990

A:Title: Identification of five putative yeast RNA helicase genes.
 A:Reference number: A34848; NUID:90160368; PMID:2406722

A:Accession: C34848
 A:Molecule type: DNA

A:Residues: 192-380, 'I', 382 <CHA>
 A:Genetics:

A:Gene: SGD:HCA4
 A:Cross-references: SGD:S0003570; MIPS:YJL033w

A:Map position: 10L
 C:Keywords: ATP; nucleotide binding; P-loop

F:85-92/Region: nucleotide-binding motif A (P-loop)
 F:190-195/Region: nucleotide-binding motif B

F:194-197/Region: DEAD motif

Query Match 58.2%; Score 39; DB 2; Length 770;
 Best Local Similarity 70.0%; Pred. No. 11e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGQ 11
 DB 142 FSAGLVGK 151

RESULT 20
 F83386
 hypothetical protein PA2070 [imported] - Pseudomonas aeruginosa (strain PA01)

A:Reference number: Z16562; MUID:97351564; PMID:9207846
A:Accession: T09139
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-249 <1TO>
A:Cross-references: UNIPROT:Q24362; EMBL:D71873; NID:G2285801; PIDN:BA21651.1; PID:G228
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 56.7%; Score 38; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 25
G84667
206 proteasome subunit C8 (PAG1/PRC8 ARATH) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84667
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q23715; GB:AE002093; NID:G3865332; PIDN:AACT7860.1; GSPDB:GN
C:Genetics:
A:Gene: Atg27020
A:Map position: 2
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 56.7%; Score 38; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 26
A84747
hypothetical protein Atg233560 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84747
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84747
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <STO>
A:Cross-references: UNIPROT:Q22806; GB:AE002093; NID:G2459438; PIDN:AA80673.1; GSPDB:GN
C:Genetics:
A:Gene: Atg233560
A:Map position: 2

Query Match 56.7%; Score 38; DB 2; Length 272;
Best Local Similarity 63.6%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGG 11
DB 215 EFGSWLMGGR 225

RESULT 27
AD2715
ABC transporter, membrane spanning protein Atu1125 [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2715
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erage, G.; Gillet, W.; Grant, C.; Guenheuer, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <KUR>
A:Cross-references: UNIPROT:Q8UGB3; GB:AE008688; PIDN:AA42138.1; PID:G17739523; GSPDB:GT
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu1125
A:Map position: circular chromosome

Query Match 56.7%; Score 38; DB 2; Length 298;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGG 9
DB 227 EFGAGLVGG 235

RESULT 28
T06385
probable Fe(II) transport protein, root - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06385
R:Cohen, C.K.; Fox, T.C.; Garvin, D.F.; Kochian, L.V.
Plant Physiol. 116, 1063-1072, 1998
A>Title: The role of iron-deficiency stress responses in stimulating heavy-metal transpor
A:Reference number: Z15642
A:Accession: T06385
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <COH>
A:Cross-references: UNIPROT:Q65348; EMBL:AF065444; NID:G3153888; PIDN:AACT17441.1; PID:G33
A:Experimental source: cultivar Sparkle
C:Genetics:
A:Gene: Rf1
C:Superfamily: Arabidopsis thaliana zinc transporter ZIP1

Query Match 56.7%; Score 38; DB 2; Length 348;
Best Local Similarity 58.3%; Pred. No. 74;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
DB 87 FAAGITLGGFM 98

RESULT 29
T28954
hypothetical protein F28A12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28954

us-09-462-416-1.rpr

Fri Dec 10 08:14:22 2004

R.Sammons, L.; Murray, J.
submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid F28A12.

A:Reference number: Z20547

A:Accession: F28954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-389 <SMA>

A:Cross-references: UNIPROT:Q22972; EMBL:U64851; PIDN:AA047989.1; GSPDB:GN00023; CESP:F2

A:Experimental source: strain Bristol N2; clone F28A12

A:Genetics:

A:Gene: CESP:F28A12.4

A:Map position: 5

A:Introns: 104/2; 147/3; 175/3; 258/3; 301/3; 341/3

C:Superfamily: pepsin

Query Match 56.7%; Score 38; DB 2; Length 389;

Best Local Similarity 58.3%; Pred. No. 83;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFGAGLVGQFM 13

Db 357 FGPSWILGQFPM 368

RESULT 30

T40924

nuclear localization protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T40924

R:Volckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 1999

A:Reference number: Z21957

A:Accession: T40924

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-390 <VOL>

A:Cross-references: UNIPROT:Q94522; EMBL:AL035218; PIDN:CAA22826.1; GSPDB:GN00068; SPDB:

A:Experimental source: strain 972H; cosmid cl281

A:Genetics:

A:Gene: SPDB:SPCC1281.05

A:Map position: 3

Query Match 56.7%; Score 38; DB 2; Length 390;

Best Local Similarity 54.5%; Pred. No. 83;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVGQ 11

Db 189 EFGARIVGGR 199

RESULT 31

G97496

integral membrane protein (A0727047) [imported] - Agrobacterium tumefaciens (strain C58,

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: G97496

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2233-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G97496

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: UNIPROT:Q8UGB3; GB:AB07869; PIDN:AA06928.1; PID:g15156158; GSPDB:G

C:Genetics:

A:Gene: AGR_C_2083

A:Map position: circular chromosome

Query Match 56.7%; Score 38; DB 2; Length 494;

Best Local Similarity 77.8%; Pred. No. 16+02; 1; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVG 9

Db 423 EFGAGLVFG 431

RESULT 32

A03463

hypothetical membrane spanning protein BME1691 [imported] - Brucella melitensis (strain

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A03463

R:DelVecchio, V.G.; Kaput, V.; Redkar, R.U.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.

; Marun, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: A03463

A:Accession: A03463

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-630 <NUR>

A:Cross-references: UNIPROT:Q8YF36; GB:AB008917; PIDN:AA052872.1; PID:g17983715; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME1691

A:Map position: 1

Query Match 56.7%; Score 38; DB 2; Length 630;

Best Local Similarity 87.5%; Pred. No. 1.3e+02; 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAGLVGG 10

Db 144 GAGLVGG 151

RESULT 33

G96498

hypothetical protein T10P12.2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: G96498

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Comar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.

A:Authors: Selzberg, S.L.; Schwartz, J.R.; Shinn, P.; Davis, R.W.

ker, M.; Wu, D.; Yu, D.; Yu, D.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A06141; MUID:21016719; PMID:11130712

A:Accession: G96498

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-748 <TGO>

A:Cross-references: UNIPROT:Q9XIG6; GB:AB005173; MID:95080761; PIDN:AA039271.1; GSPDB:GN

A:Genetics:

A:Gene: T10P12.2

A:Map position: 1

Query Match 56.7%; Score 38; DB 2; Length 748;

Best Local Similarity 53.8%; Pred. No. 1.5e+02; 3; Indels 0; Gaps 0;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVGQFM 13

Db 265 QFGSVKVGQF 277

RESULT 34
AE0614
probable competence-related protein STY0984 [imported] - *Salmonella enterica* subsp. ente
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:Note: this species has also been called *Salmonella typh*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
C:Accession: AE0614
R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nucleotide 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0614
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-754 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05383.1; PID:gl6502146; GSPDB:GN00176
C:Genetics:
A:Gene: STY0984
C:Superfamily: competence protein ComEC

Query Match
Best Local Similarity 56.7%; Score 38; DB 2; Length 754;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGLVGGGF 12
|||: |||
Db 240 AGLRGQGF 248

RESULT 35
S76592
5-methyltetrahydrofolate-homocysteine S-methyltransferase (EC 2.1.1.13) [similarity] - S
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76592
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1195 <KAN>
A:Cross-references: UNIPROT:Q55786; EMBL:D64002; GB:AB001339; NID:gl001612; PIDN:BAH1043
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology
C:Keywords: methyltransferase
F:737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted

Query Match
Best Local Similarity 56.7%; Score 38; DB 2; Length 1195;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLVG 9
|||: |||
Db 456 EYGAAGVIG 464

RESULT 36
D64012
hypothetical protein H10704 - *Haemophilus influenzae* (strain Rd KW20)
C:Species: *Haemophilus influenzae*
A:Variety: strain Rd KW20
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: D64012; T09409
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Georgiagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C
A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: D64012
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-61 <RTGR>
A:Cross-references: UNIPROT:P44040; GB:U32753; GB:L42023; NID:gl573701; PIDN:AAC2367.1;
C:Genetics:
A:Note: H10704

Query Match
Best Local Similarity 55.2%; Score 37; DB 2; Length 61;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GAGLVGGQFM 13
|||: |||
Db 38 GTGAVAGSFM 48

RESULT 37
J50297
infection structure-specific protein - rust fungus (*Uromyces appendiculatus*)
C:Species: *Uromyces appendiculatus*
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: J50297
R:Bhairi, S.M.; Staples, R.C.; Freve, P.; Yoder, O.C.
Gene 81, 237-243, 1989
A:Title: Characterization of an infection structure-specific gene from the rust fungus *U*
A:Reference number: J50297; MUID:90034196; PMID:2806914
A:Accession: J50297
A:Molecule type: DNA
A:Residues: 1-150 <BHA>
A:Cross-references: UNIPROT:P14777
C:Comment: This protein is involved in the development of infection structures and the cc
C:Genetics:
A:Gene: INF24

Query Match
Best Local Similarity 55.2%; Score 37; DB 2; Length 150;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EFGAGLVGGQGF 12
|||: |||
Db 24 EFGAGLVGGQGF 34

RESULT 38
AH1737
NADH-dependent FMN reductase homolog lin2445 [imported] - *Listeria innocua* (strain Clp1)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1737
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duessegger, O.; Ertlan, K.D.; Fehli, H.;
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitouram, A.; Mat
ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voess, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <Gla>
A:Cross-references: UNIPROT:Q92877; GB:AL592022; PIDN:CMC97672.1; PID:gl6414967; GSPDB:GR
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin2445

